NiceProt View of Swiss-Prot: Q45983

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Entry information

Entry name	**PTMA_CAMCO**
Primary accession number	**Q45983**
Secondary accession numbers	None
Entered in Swiss-Prot in	Release 36, July 1998
Sequence was last modified in	Release 36, July 1998
Annotations were last modified in	Release 44, July 2004

Name and origin of the protein

Protein name	**Posttranslational flagellin modification protein A**
Synonyms	None
Gene name	**Name: ptmA**
From	Campylobacter coli [TaxID: 195]
Taxonomy	Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter.

References

[1] SEQUENCE FROM NUCLEIC ACID.
STRAIN=VC167;
MEDLINE=96423180;PubMed=8825781 [NCBI, ExPASy, EBI, Israel, Japan]
Guerry P., Doig P., Alm R.A., Burr D.H., Kinsella N., Trust T.J.;
"Identification and characterization of genes required for post-translational modification of Campylobacter coli VC167 flagellin.";
Mol. Microbiol. 19:369-378(1996).

Comments

- ***FUNCTION***: Required for biosynthesis of LAH modification in the post-translational modification of Campylobacter coli flagellin.
- ***SIMILARITY***: Belongs to the short-chain dehydrogenases/reductases (SDR) family.

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license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch)

Cross-references

EMBL	AY102621; AAM76282.1; -.[EMBL / GenBank / DDBJ] [CoDingSequence]
PIR	S70686; S70686.
InterPro	IPR002198; ADH_short. IPR002347; Adh_short_C2. Graphical view of domain structure.
Pfam	PF00106; adh_short; 1. Pfam graphical view of domain structure.
PRINTS	PR00081; GDHRDH.
PROSITE	PS00061; ADH_SHORT; FALSE_NEG.
ProDom	[Domain structure / List of seq. sharing at least 1 domain]
HOBACGEN	[Family / Alignment / Tree]
BLOCKS	Q45983.
ProtoNet	Q45983.
ProtoMap	Q45983.
PRESAGE	Q45983.
DIP	Q45983.
ModBase	Q45983.
SMR	Q45983; 46045E806390D69F.
SWISS-2DPAGE	Get region on 2D PAGE.
UniRef	View cluster of proteins with at least 50% / 90% identity.

Keywords

Oxidoreductase.

Features

Feature table viewer

Key	From	To	Length	Description
ACT_SITE	168	168		*By similarity.*

Sequence information

Length: **256 AA** Molecular weight: **28489 Da** CRC64: **46045E806390D69F** [This is a checksum on the sequence]

```
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         |          |          |          |          |          |
MLENKIIFVA GACGRIGKAL CKKILQNKGI AILADINENH LSILKTELEN EFKKELLSLR

        70         80         90        100        110        120
         |          |          |          |          |          |
LDITSKESLN CAIDQAFEKY SKIDGFVNSS YPVGKDWGKI AYYEASYEQI CESLNLHLGG

       130        140        150        160        170        180
         |          |          |          |          |          |
FILASQEFVK FFKKQSYGNI INLSSIMGVF APKFENYENT TMQSSLEYSV IKAGINHLGA

       190        200        210        220        230        240
         |          |          |          |          |          |
WLAKELFNTN IRVNTLASGG ILDNQANIFL EKYRKCCASK GMLDAEDICG TLVFLLSDES
```

```
       250
        |
KFVTGQTLVV DDGWGL
```

Q45983 in FASTA format

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Sequence analysis tools: ProtParam, ProtScale, Compute pI/Mw, PeptideMass, PeptideCutter, Dotlet (Java)

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NiceProt View of Swiss-Prot: P27053

Printer-friendly view | Submit update | Quick BlastP search

[Entry info] [Name and origin] [References] [Comments] [Cross-references] [Keywords] [Features] [Sequence] [Tools]

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Entry information

Entry name	**FLAA_CAMCO**
Primary accession number	**P27053**
Secondary accession numbers	None
Entered in Swiss-Prot in	Release 23, August 1992
Sequence was last modified in	Release 34, October 1996
Annotations were last modified in	Release 44, July 2004

Name and origin of the protein

Protein name	**Flagellin A**
Synonyms	None
Gene name	**Name: flaA**
From	Campylobacter coli [TaxID: 195]
Taxonomy	Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter.

References

[1] SEQUENCE FROM NUCLEIC ACID.
STRAIN=VC167 T2;
MEDLINE=91310584;PubMed=1856171 [NCBI, ExPASy, EBI, Israel, Japan]
Guerry P., Alm R.A., Power M.E., Logan S.M., Trust T.J.;
"Role of two flagellin genes in Campylobacter motility.";
J. Bacteriol. 173:4757-4764(1991).

Comments

- ***FUNCTION***: Flagellin is the subunit protein which polymerizes to form the filaments of bacterial flagella.
- ***SUBUNIT***: Heteropolymer of flaA and flaB. A flagellar filament composed exclusively of flaA is indistinguishable in length from that of the wild type and shows a slight reduction in motility. The flagellar filament composed exclusively of the flaB is severely truncated in length and greatly reduced in motility. Thus, while both flagellins are not necessary for motility, both are required for a fully active flagellar filament.
- ***SIMILARITY***: Belongs to the bacterial flagellin family.

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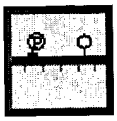
Cross-references

EMBL	M64670; AAA23022.1; -.[EMBL / GenBank / DDBJ] [CoDingSequence] M64671; AAA23026.1; -.[EMBL / GenBank / DDBJ] [CoDingSequence]
PIR	A42474; A42474.
HSSP	P06179; 1UCU. [HSSP ENTRY / PDB]
InterPro	IPR001029; Flagellin_C. IPR010810; Flagellin_IN. IPR001492; Flagellin_N. Graphical view of domain structure.
Pfam	PF00700; Flagellin_C; 1. PF07196; Flagellin_IN; 2. PF00669; Flagellin_N; 1. Pfam graphical view of domain structure.
PRINTS	PR00207; FLAGELLIN.
ProDom	PD000316; Flagellin_C; 2. [Domain structure / List of seq. sharing at least 1 domain]
HOBACGEN	[Family / Alignment / Tree]
BLOCKS	P27053.
ProtoNet	P27053.
ProtoMap	P27053.
PRESAGE	P27053.
DIP	P27053.
ModBase	P27053.
SMR	P27053; BD97DFF6CD099004.
SWISS-2DPAGE	Get region on 2D PAGE.
UniRef	View cluster of proteins with at least 50% / 90% identity.

Keywords

Flagellum.

Features

 Feature table viewer

Key	From	To	Length	Description
INIT_MET	0	0		*By similarity.*
VARIANT	201	202	2	DS -> QN.

Sequence information

Length: **572** **AA** Molecular weight: **58880** **Da** CRC64: **BD97DFF6CD099004** [This is a checksum on the sequence]

```
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         |          |          |          |          |          |
GFRINTNVAA LNAKANSDLN SRALDQSLSR LSSGLRINSA ADDASGMAIA DSLRSQANTL
```

```
         70          80          90         100         110         120
          |           |           |           |           |           |
GQAISNGNDA LGILQTADKA MDEQLKILDT IKTKATQAAQ DGQSLKTRTM LQADINRLME

        130         140         150         160         170         180
          |           |           |           |           |           |
ELDNIANTTS FNGKQLLSGG FTNQEFQIGS SSNQTIKASI GATQSSKIGV TRFETGSQSF

        190         200         210         220         230         240
          |           |           |           |           |           |
SSGTVGLTIK NYNGIEDFKF DSVVISTSVG TGLGALAEEI NRNADKTGIR ATFDVKSVGA

        250         260         270         280         290         300
          |           |           |           |           |           |
YAIKAGNTSQ DFAINGVVIG KVDYSDGDEN GSLISAINAV KDTTGVQASK DENGKLVLTS

        310         320         330         340         350         360
          |           |           |           |           |           |
ADGRGIKITG SIGVGAGILH TENYGRLSLV KNDGRDINIS GTGLSAIGMG ATDMISQSSV

        370         380         390         400         410         420
          |           |           |           |           |           |
SLRESKGQIS AANADAMGFN AYNGGGAKQI IFASSIAGFM SQAGSGFSAG SGFSVGSGKN

        430         440         450         460         470         480
          |           |           |           |           |           |
YSAILSASIQ IVSSARSISS TYVVSTGSGF SAGSGNSQFA ALRISTVSAH DETAGVTTLK

        490         500         510         520         530         540
          |           |           |           |           |           |
GAMAVMDIAE TAITNLDQIR ADIGSVQNQI TSTINNITVT QVNVKSAESQ IRDVDFASES

        550         560         570
          |           |           |
ANYSKANILA QSGSYAMAQA NSSQQNVLRL LQ
```

P27053 in FASTA format

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BLAST submission on ExPASy/SIB or at NCBI (USA)

Sequence analysis tools: ProtParam, ProtScale, Compute pI/Mw, PeptideMass, PeptideCutter, Dotlet (Java)

ScanProsite, MotifScan

Search the SWISS-MODEL Repository

NiceProt View of TrEMBL: O30688

Note: most headings are clickable, even if they don't appear as links. They link to the user manual or other documents.

Entry information

Entry name	**O30688**
Primary accession number	**O30688**
Secondary accession numbers	None
Entered in TrEMBL in	Release 05, January 1998
Sequence was last modified in	Release 05, January 1998
Annotations were last modified in	Release 24, June 2003

Name and origin of the protein

Protein name	**Flagellin A [Fragment]**
Synonyms	None
Gene name	**Name: flaA**
From	Campylobacter coli [TaxID: 195]
Taxonomy	Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter.

References

[1] SEQUENCE FROM NUCLEIC ACID.
STRAIN=D1159;
Meinersmann R.J., Helsel L.O., Fields P.I., Hiett K.L.;
"Discrimination of Campylobacter jejuni by fla gene sequencing.";
J. Clin. Microbiol. 0:0-0(1997).

Comments

None

Cross-references

EMBL: AF015091; AAB69353.1; -.[EMBL / GenBank / DDBJ] [CoDingSequence]

GO:
- GO:0009420; Cellular component: flagellar filament (sensu Bacteria) *(inferred from electronic annotation).*
- GO:0005198; Molecular function: structural molecule activity *(inferred from electronic annotation).*
- GO:0001539; Biological process: ciliary or flagellar motility *(inferred from electronic annotation).*

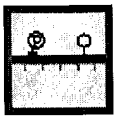
IPR001492; Flagellin_N.

InterPro	Graphical view of domain structure.
Pfam	PF00669; Flagellin_N; 1. Pfam graphical view of domain structure.
ProtoMap	O30688.
PRESAGE	O30688.
ModBase	O30688.
SMR	O30688; A1EBB1B61699B04D.
SWISS-2DPAGE	Get region on 2D PAGE.
UniRef	View cluster of proteins with at least 50% / 90% identity.

Keywords

Flagellum.

Features


Feature table viewer

Key	From	To	Length	Description
NON_TER	1	1		
NON_TER	89	89		

Sequence information

Length: **89 AA** [This is the length of the partial sequence]

Molecular weight: **9630 Da** [This is the MW of the partial sequence]

CRC64: **A1EBB1B61699B04D** [This is a checksum on the sequence]

```
         10          20          30          40          50          60
          |           |           |           |           |           |
QDGQSLKTRT MLQADINRLM EELDNIANTT SFNGKQLLSG NFINQEFQIG ASSNQTVKAT

         70          80
          |           |
IGATQSSKIG LTRFETGGRI SSSGEVQFT
```

O30688 in FASTA format

View entry in original TrEMBL format
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Request for annotation of this TrEMBL entry

BLAST submission on ExPASy/SIB or at NCBI (USA)

Sequence analysis tools: ProtParam, ProtScale, Compute pI/Mw, PeptideMass, PeptideCutter, Dotlet (Java)

ScanProsite, MotifScan

Search the SWISS-MODEL Repository

NiceProt View of TrEMBL: Q9WW79

Note: most headings are clickable, even if they don't appear as links. They link to the user manual or other documents.

Entry information

Entry name	**Q9WW79**
Primary accession number	**Q9WW79**
Secondary accession numbers	None
Entered in TrEMBL in	Release 12, November 1999
Sequence was last modified in	Release 12, November 1999
Annotations were last modified in	Release 19, December 2001

Name and origin of the protein

Protein name	**Flagellin A [Fragment]**
Synonyms	None
Gene name	**Name: flaA**
From	Campylobacter coli [TaxID: 195]
Taxonomy	Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter.

References

[1] SEQUENCE FROM NUCLEIC ACID.
Studer E., Dohmke M., Wegmueller B., Luethy J., Schmid S., Candrian U.;
"RFLP and sequence analysis of Campylobacter jejuni and Campylobacter coli PCR products amplified directly from environmental samples.";
Food Sci. Technol. 31:337-345(1998).

[2] SEQUENCE FROM NUCLEIC ACID.
Studer E.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.

Comments

None

Cross-references

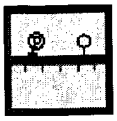
ProtoMap	Q9WW79.
PRESAGE	Q9WW79.
ModBase	Q9WW79.
SMR	Q9WW79; C7C0EFB7A1739156.
SWISS-2DPAGE	Get region on 2D PAGE.

UniRef View cluster of proteins with at least 50% / 90% identity.

Keywords

Flagellum.

Features

 Feature table viewer

Key	From	To	Length	Description
NON_TER	1	1		

Sequence information

Length: **14 AA** [This is the length of the partial sequence]

Molecular weight: **1611 Da** [This is the MW of the partial sequence]

CRC64: **C7C0EFB7A1739156** [This is a checksum on the sequence]

```
         10
          |
QANSVQQNVL RLLQ
```

Q9WW79 in FASTA format

View entry in original TrEMBL format
View entry in raw text format (no links)
Request for annotation of this TrEMBL entry

BLAST BLAST submission on ExPASy/SIB or at NCBI (USA)

Sequence analysis tools: ProtParam, ProtScale, Compute pI/Mw, PeptideMass, PeptideCutter, Dotlet (Java)

ScanProsite, MotifScan

Search the SWISS-MODEL Repository

NiceProt View of TrEMBL: Q46009

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[Entry info] [Name and origin] [References] [Comments] [Cross-references] [Keywords] [Features] [Sequence] [Tools]

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Entry information

Entry name	**Q46009**
Primary accession number	**Q46009**
Secondary accession numbers	None
Entered in TrEMBL in	Release 01, November 1996
Sequence was last modified in	Release 01, November 1996
Annotations were last modified in	Release 26, March 2004

Name and origin of the protein

Protein name	**Flagellin**
Synonyms	None
Gene name	None
From	Campylobacter coli [TaxID: 195]
Taxonomy	Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter.

References

[1] SEQUENCE FROM NUCLEIC ACID.
STRAIN=VC167;
MEDLINE=89255058;PubMed=2722741 [NCBI, ExPASy, EBI, Israel, Japan]
Logan S.M., Trust T.J., Guerry P.;
"Evidence for posttranslational modification and gene duplication of Campylobacter flagellin.";
J. Bacteriol. 171:3031-3038(1989).

Comments

None

Cross-references

EMBL	M26945; AAA23021.1; -.[EMBL / GenBank / DDBJ] [CoDingSequence]
PIR	A44757; A44757.
GO	GO:0009420; Cellular component: flagellar filament (sensu Bacteria) *(inferred from electronic annotation).*
	GO:0005198; Molecular function: structural molecule activity *(inferred from electronic annotation).*
	GO:0001539; Biological process: ciliary or flagellar motility *(inferred from electronic*

annotation).

InterPro	IPR001029; Flagellin_C. IPR010810; Flagellin_IN. IPR001492; Flagellin_N. Graphical view of domain structure.
Pfam	PF00700; Flagellin_C; 1. PF07196; Flagellin_IN; 2. PF00669; Flagellin_N; 1. Pfam graphical view of domain structure.
PRINTS	PR00207; FLAGELLIN.
ProDom	PD000316; Flagellin_C; 1. [Domain structure / List of seq. sharing at least 1 domain]
HOBACGEN	[Family / Alignment / Tree]
ProtoMap	Q46009.
PRESAGE	Q46009.
ModBase	Q46009.
SMR	Q46009; DA7CCBB23588EA7A.
SWISS-2DPAGE	Get region on 2D PAGE.
UniRef	View cluster of proteins with at least 50% / 90% identity.

Keywords

Flagellum.

Features

None

Sequence information

Length: **572 AA** Molecular weight: **58982 Da** CRC64: **DA7CCBB23588EA7A** [This is a checksum on the sequence]

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          |          |          |          |          |          |
MGFRINTNVA ALNAKANSDL NSRALDQSLS RLSSGLRINS AADVASGMAI ADSLRSQANT

         70         80         90        100        110        120
          |          |          |          |          |          |
LGQAISNGND ALGILQTADK AMDEQLKILD TIKTKATQAA EDGQSLKTRT MLQADINRLM

        130        140        150        160        170        180
          |          |          |          |          |          |
EELDNIANTT SFNGKQLLSG GFTNQEFQIG SSSNQTIKAS IGATQSSKIG VTRLNRFTKF

        190        200        210        220        230        240
          |          |          |          |          |          |
SSGTVGLTIK NYNGIEDFKF DSVVISTSVG TGLGALAEEI NRNADKTGIR ATFDLKSVGA

        250        260        270        280        290        300
          |          |          |          |          |          |
YAIKAGNTSQ DFAINGVVIG KVDYSDGDEN GSLISAINAV KDTTGVQASK DENGKLVLTS

        310        320        330        340        350        360
          |          |          |          |          |          |
ADGRGIKITG SIGVGAGILH TENYGRLSLV KNDGRDINIS GTGFSAIGMG ATDMISQSSV
```

```
        370         380         390         400         410         420
         |           |           |           |           |           |
SLRESKGQIS AANADAMGFN AYNGGGAKQI IFASSIAGFM SQAGSGFSAG SGFSVGSGKN

        430         440         450         460         470         480
         |           |           |           |           |           |
YSAILSASIQ IVSSAASISS TYVVSTGSGF SAGSGNSQFA ALRISTVSAH DETAGVTTLK

        490         500         510         520         530         540
         |           |           |           |           |           |
GAMAVMDIAE TAITNLDQIR ADIGSVQNQI TSTINNITVT QVNVKSAESQ IRDVDFASES

        550         560         570
         |           |           |
ANYSKANILA QSGSYAMAQA NSSQQNVLRL LQ
```

Q46009 in FASTA format

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BLAST BLAST submission on ExPASy/SIB or at NCBI (USA)

Sequence analysis tools: ProtParam, ProtScale, Compute pI/Mw, PeptideMass, PeptideCutter, Dotlet (Java)

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EBI **Dbfetch**

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ID   CCFLA01    standard; genomic DNA; PRO; 1719 BP.
XX
AC   M26945;
XX
SV   M26945.1
XX
DT   23-NOV-1989 (Rel. 21, Created)
DT   23-DEC-2002 (Rel. 74, Last updated, Version 4)
XX
DE   Campylobacter coli flagellin gene, complete cds.
XX
KW   .
XX
OS   Campylobacter coli
OC   Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC   Campylobacteraceae; Campylobacter.
XX
RN   [1]
RP   1-1719
RX   MEDLINE; 89255058.
RX   PUBMED; 2722741.
RA   Logan S.M., Trust T.J., Guerry P.;
RT   "Evidence for posttranslational modification and gene duplication of
RT   Campylobacter flagellin";
RL   J. Bacteriol. 171(6):3031-3038(1989).
XX
FH   Key             Location/Qualifiers
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```

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FT                   GTGFSAIGMGATDMISQSSVSLRESKGQISAANADAMGFNAYNGGGAKQIIFASSIAG
FT                   MSQAGSGFSAGSGFSVGSGKNYSAILSASIQIVSSAASISSTYVVSTGSGFSAGSGNS
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FT                   TVTQVNVKSAESQIRDVDFASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ"
XX
SQ   Sequence 1719 BP; 563 A; 284 C; 365 G; 507 T; 0 other;
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EBI **Dbfetch**

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SV   M64670.1
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DT   01-MAY-1991 (Rel. 28, Created)
DT   05-JUL-1999 (Rel. 60, Last updated, Version 3)
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DE   C.coli flagellin (flaA and flaB) genes, complete cds.
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KW   flagellin.
XX
OS   Campylobacter coli
OC   Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC   Campylobacteraceae; Campylobacter.
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RN   [1]
RP   1-4200
RX   MEDLINE; 91310584.
RX   PUBMED; 1856171.
RA   Guerry P., Alm R.A., Power M.E., Logan S.M., Trust T.J.;
RT   "Role of two flagellin genes in Campylobacter motility";
RL   J. Bacteriol. 173(15):4757-4764(1991).
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Search in Swiss-Prot and TrEMBL for: coli campylobacter flagellin

Swiss-Prot Release 44.4 of 31-Aug-2004
TrEMBL Release 27.4 of 31-Aug-2004

- Number of sequences found in Swiss-Prot$_{(4)}$ and TrEMBL$_{(5)}$: **9**
- Note that the selected sequences can be saved to a file to be later retrieved; to do so, go to the bottom of this page.
- For more directed searches, you can use the Sequence Retrieval System SRS.

Search in Swiss-Prot: There are matches to 4 out of 158010 entries

FLAA_CAMCO (**P27053**)
Flagellin A. {GENE: Name=flaA} - Campylobacter coli
FLAB_CAMCO (**P18245**)
Flagellin B (Flagellin N). {GENE: Name=flaB} - Campylobacter coli
PTMA_CAMCO (**Q45983**)
Posttranslational flagellin modification protein A. {GENE: Name=ptmA} - Campylobacter coli
PTMB_CAMCO (**Q45982**)
Posttranslational flagellin modification protein B. {GENE: Name=ptmB} - Campylobacter coli

---

Search in TrEMBL: There are matches to 5 out of 1377572 entries

O30688
Flagellin A (Fragment) {GENE:Name=flaA} - Campylobacter coli
Q46009
Flagellin - Campylobacter coli
Q8G9F1
Flagellin (Fragment) {GENE:Name=flaA} - Campylobacter coli
Q8G9F3
Flagellin (Fragment) {GENE:Name=flaA} - Campylobacter coli
Q9WW79
Flagellin A (Fragment) {GENE:Name=flaA} - Campylobacter coli

New Search
in Swiss-Prot/TrEMBL by AC, ID, description, gene name, organism
Please do NOT use any boolean operators (and, or, etc.)

If you would like to retrieve all the Swiss-Prot/TrEMBL entries contained in this list , you can enter a file name. These entries will then be saved to a file under this name in the directory `outgoing` of the ExPASy anonymous ftp server, from where you can download it. (Please note that this temporary file will only be kept for 1 week.)

File name:

Format: (•) Swiss-Prot ( ) Fasta

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ExPASy Home page | Site Map | Search ExPASy | Contact us | Proteomics tools | Swiss-Prot

Search Swiss-Prot/TrEMBL for coli campylobacter flage Go Clear

==========

Welcome to the SIB BLAST Network Service

If results of this search are reported or published, please mention that the computation was performed at the SIB using the BLAST network service. The SIB BLAST network service uses a server developed at SIB and the NCBI BLAST 2 software.

In case of problems, please read the online BLAST help.
If your question is not covered, please contact <helpdesk@expasy.org>.

NCBI BLAST program reference [PMID:9254694]:
Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W., Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25:3389-3402(1997).

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Query length: 420 AA (of which 5% low-complexity regions filtered out)
Date run: 2004-09-02 16:29:13 UTC+0100 on sib-gm1.unil.ch
Program: NCBI BLASTP 1.5.4-Paracel [2003-06-05]
Database: EXPASY/UniProt
1,544,870 sequences; 494,584,931 total letters

Taxonomic view | NiceBlast view | Printable view

List of potentially matching sequences

Send selected sequences to Clustal W (multiple alignment) Submit Query

Select up to...

☐ Include query sequence

	Db	AC	Description	Score	E-value
☐	sp	P27053	FLAA_CAMCO Flagellin A [flaA] [Campylobacter coli]	750	0.0
☐	tr	Q84IB9	Flagellin (Fragment) [flaA] [Campylobacter jejuni]	736	0.0
☐	tr	Q46009	Flagellin [Campylobacter coli]	724	0.0
☐	sp	P18245	FLAB_CAMCO Flagellin B (Flagellin N) [flaB] [Campyloba...	723	0.0
☐	tr	Q9RPY6	Flagellin A [flaA] [Campylobacter jejuni]	722	0.0
☐	tr	Q99QL6	Flagellin A (Fragment) [flaA] [Campylobacter jejuni]	702	0.0
☐	tr	Q99Q27	Flagellin A (Fragment) [flaA] [Campylobacter jejuni]	696	0.0
☐	tr	Q93NL6	Flagellin A (Fragment) [flaA] [Campylobacter jejuni]	687	0.0
☐	tr	Q93NL9	Flagellin A (Fragment) [flaA] [Campylobacter jejuni]	687	0.0
☐	sp	P22251	FLA2_CAMJE Flagellin A [flaA] [Campylobacter jejuni]	674	0.0

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☐	tr O85179 Flagellin A [flaA] [Campylobacter jejuni]	674	0.0
☐	tr Q9R950 Flagellin A [flaA] [Campylobacter jejuni]	672	0.0
☐	tr Q9RF26 Chimeric flagellin A/B [Campylobacter jejuni]	670	0.0
☐	tr Q9R953 Flagellin A [flaA] [Campylobacter jejuni]	669	0.0
☐	tr O85183 Flagellin A [flaA] [Campylobacter jejuni]	667	0.0
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☐	tr Q7X516 FlaB [flaB] [Campylobacter jejuni]	657	0.0
☐	tr Q6L5K6 Flagellin (Fragment) [flaA] [Campylobacter lari]	608	e-173
☐	tr Q6L5K7 Flagellin (Fragment) [flaA] [Campylobacter lari]	606	e-172
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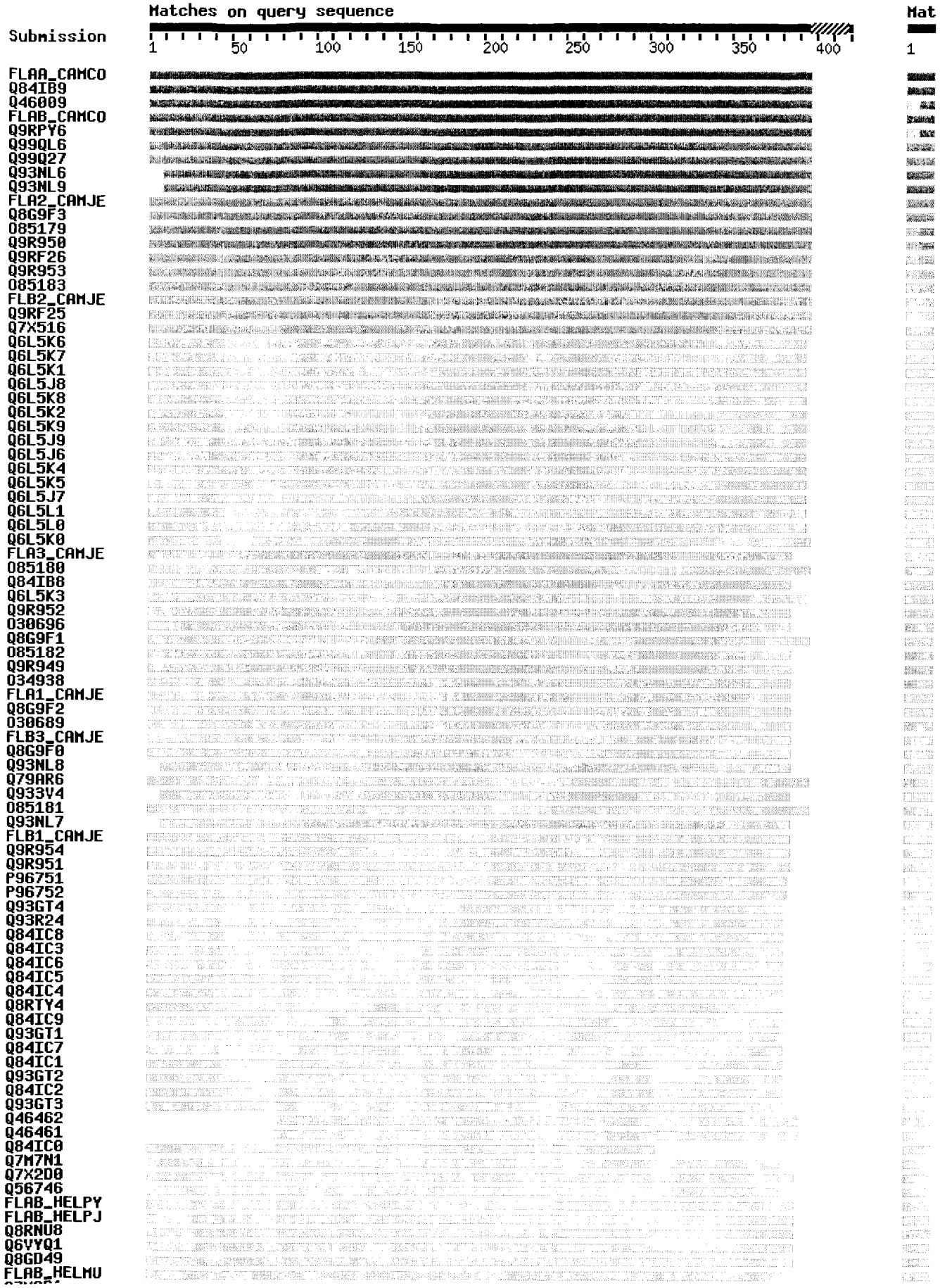
tr Q93R24	Flagellin (Fragment) [flaA] [Campylobacter lari]	488	e-137
tr Q84IC8	Flagellin (Fragment) [flaA] [Campylobacter lari]	483	e-135
tr Q84IC3	Flagellin (Fragment) [flaA] [Campylobacter lari]	482	e-135
tr Q84IC6	Flagellin (Fragment) [flaA] [Campylobacter lari]	481	e-135
tr Q84IC5	Flagellin (Fragment) [flaA] [Campylobacter lari]	481	e-135
tr Q84IC4	Flagellin (Fragment) [flaA] [Campylobacter lari]	481	e-135
tr Q8RTY4	Flagellin (Fragment) [flaA] [Campylobacter lari]	479	e-134
tr Q84IC9	Flagellin (Fragment) [flaA] [Campylobacter lari]	479	e-134
tr Q93GT1	Flagellin (Fragment) [flaA] [Campylobacter lari]	478	e-134
tr Q84IC7	Flagellin (Fragment) [flaA] [Campylobacter lari]	478	e-133
tr Q84IC1	Flagellin (Fragment) [flaA] [Campylobacter lari]	473	e-132
tr Q93GT2	Flagellin (Fragment) [flaA] [Campylobacter lari]	473	e-132
tr Q84IC2	Flagellin (Fragment) [flaA] [Campylobacter lari]	471	e-131
tr Q93GT3	Flagellin (Fragment) [flaA] [Campylobacter lari]	463	e-129
tr Q46462	Flagellin (Fragment) [fla2] [Campylobacter upsaliensis]	453	e-126
tr Q46461	Flagellin (Fragment) [fla1] [Campylobacter upsaliensis]	444	e-123
tr Q84IC0	Flagellin (Fragment) [flaA] [Campylobacter lari]	424	e-117
tr Q7M7N1	FLAGELLIN B [FLAB] [Wolinella succinogenes]	383	e-105
tr Q7X2D0	Flagellin B [flaB] [Helicobacter pylori (Campylobacter...	380	e-104
tr Q56746	Flagellin [flag] [Wolinella succinogenes]	379	e-104
sp Q07911	FLAB_HELPY Flagellin B (Flagellin N) [flaB] [Helicobac...	376	e-103
sp Q9ZMV8	FLAB_HELPJ Flagellin B (Flagellin N) [flaB] [Helicobac...	376	e-103
tr Q8RNU8	Flagellin B subunit [flaB] [Helicobacter pylori (Campy...	376	e-103
tr Q6VYQ1	Flagellin B [flaB] [Helicobacter pylori (Campylobacter...	376	e-103
tr Q8GD49	Flagellin [flaB] [Helicobacter pylori (Campylobacter p...	375	e-103
sp Q07910	FLAB_HELMU Flagellin B (Flagellin N) [flaB] [Helicobac...	368	e-100
tr Q7X2D1	Flagellin A [flaA] [Helicobacter pylori (Campylobacter...	365	e-100
tr Q9XB37	Flagellin B [flaB] [Helicobacter felis]	365	e-100
tr Q7TTM9	Major flagellin subunit FlaA_1 (Major flagellin subuni...	363	3e-99
sp Q03843	FLAA_HELPY Flagellin A [flaA] [Helicobacter pylori (Ca...	361	1e-98
sp Q9XB38	FLAA_HELFE Flagellin A [flaA] [Helicobacter felis]	358	1e-97
tr Q6VYQ2	Flagellin A [flaA] [Helicobacter pylori (Campylobacter...	358	1e-97
tr Q7VF81	Minor flagellin subunit FlaB [flaB] [Helicobacter hepa...	356	5e-97
sp P50612	FLAA_HELMU Flagellin A [flaA] [Helicobacter mustelae]	345	9e-94
tr Q8VN93	Flagellin B (Fragment) [flaB] [Helicobacter pylori (Ca...	335	1e-90
tr Q8VN92	Flagellin B (Fragment) [flaB] [Helicobacter pylori (Ca...	334	2e-90
tr Q93NM0	Flagellin A (Fragment) [flaA] [Campylobacter jejuni]	332	8e-90
tr Q93NM1	Flagellin A (Fragment) [flaA] [Campylobacter jejuni]	332	1e-89
tr Q8VN91	Flagellin A (Fragment) [flaA] [Helicobacter pylori (Ca...	330	2e-89
tr Q8VN90	Flagellin A (Fragment) [flaA] [Helicobacter pylori (Ca...	330	2e-89

Graphical overview of the alignments

Click here to resubmit your query after masking regions matching PROSITE profiles or Pfam HMMs

(? Help) (use ScanProsite for more details about PROSITE matches)


Matches on query sequence
Mat
Submission
1
50
100
150
200
250
300
350
400
1
FLAA_CAMCO
Q84IB9
Q46009
FLAB_CAMCO
Q9RPY6
Q99QL6
Q99Q27
Q93NL6
Q93NL9
FLA2_CAMJE
Q8G9F3
O85179
Q9R950
Q9RF26
Q9R953
O85183
FLB2_CAMJE
Q9RF25
Q7X516
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Q6L5K9
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Q6L5J6
Q6L5K4
Q6L5K5
Q6L5J7
Q6L5L1
Q6L5L0
Q6L5K0
FLA3_CAMJE
O85180
Q84IB8
Q6L5K3
Q9R952
O30696
Q8G9F1
O85182
Q9R949
O34938
FLA1_CAMJE
Q8G9F2
O30689
FLB3_CAMJE
Q8G9F0
Q93NL8
Q79AR6
Q933V4
O85181
Q93NL7
FLB1_CAMJE
Q9R954
Q9R951
P96751
P96752
Q93GT4
Q93R24
Q84IC8
Q84IC3
Q84IC6
Q84IC5
Q84IC4
Q8RTY4
Q84IC9
Q93GT1
Q84IC7
Q84IC1
Q93GT2
Q84IC2
Q93GT3
Q46462
Q46461
Q84IC0
Q7M7N1
Q7X2D0
Q56746
FLAB_HELPY
FLAB_HELPJ
Q8RNU8
Q6VYQ1
Q8GD49
FLAB_HELMU

Alignments

sp P27053 FLAA_CAMCO **Flagellin A [flaA] [Campylobacter coli]** 572 AA align

Score = 750 bits (1937), Expect = 0.0
Identities = 396/396 (100%), Positives = 396/396 (100%)

```
Query: 1   GFRINTNVAALNAKANSDLNSRALDQSLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
           GFRINTNVAALNAKANSDLNSRALDQSLSRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 1   GFRINTNVAALNAKANSDLNSRALDQSLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60

Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120
           GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME
Sbjct: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120

Query: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 180
           ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF
Sbjct: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 180

Query: 181 SSGTVGLTIKNYNGIEDFKFDSVVISTSVGTGLGALAEEINRNADKTGIRATFDVKSVGA 240
           SSGTVGLTIKNYNGIEDFKFDSVVISTSVGTGLGALAEEINRNADKTGIRATFDVKSVGA
Sbjct: 181 SSGTVGLTIKNYNGIEDFKFDSVVISTSVGTGLGALAEEINRNADKTGIRATFDVKSVGA 240

Query: 241 YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLVLTS 300
           YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLVLTS
Sbjct: 241 YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLVLTS 300

Query: 301 ADGRGIKITGSIGVGAGILHTENYGRLSLVKNDGRDINISGTGLSAIGMGATDMISQSSV 360
           ADGRGIKITGSIGVGAGILHTENYGRLSLVKNDGRDINISGTGLSAIGMGATDMISQSSV
Sbjct: 301 ADGRGIKITGSIGVGAGILHTENYGRLSLVKNDGRDINISGTGLSAIGMGATDMISQSSV 360

Query: 361 SLRESKGQISAANADAMGFNAYNGGGAKQIIFASSI 396
           SLRESKGQISAANADAMGFNAYNGGGAKQIIFASSI
Sbjct: 361 SLRESKGQISAANADAMGFNAYNGGGAKQIIFASSI 396
```

tr Q84IB9 **Flagellin (Fragment) [flaA] [Campylobacter jejuni]** 572 AA align

Score = 736 bits (1901), Expect = 0.0
Identities = 389/396 (98%), Positives = 392/396 (98%)

```
Query: 1   GFRINTNVAALNAKANSDLNSRALDQSLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
           GFRINTN AALNAKANSDLNSRALDQSLSRLSSGLRINSAADDASGMAIADSLRSQANT+
Sbjct: 1   GFRINTNGAALNAKANSDLNSRALDQSLSRLSSGLRINSAADDASGMAIADSLRSQANTM 60

Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120
           GQAISNG+DALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME
Sbjct: 61  GQAISNGDDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120

Query: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 180
           ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF
Sbjct: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 180
```

```
Query: 181 SSGTVGLTIKNYNGIEDFKFDSVVISTSVGTGLGALAEEINRNADKTGIRATFDVKSVGA 240
           SSGTVGLTIKNYNGIEDFKF +VVISTSVGTGLGALAEEINRNADKTGIRATFDVKSVGA
Sbjct: 181 SSGTVGLTIKNYNGIEDFKFQNVVISTSVGTGLGALAEEINRNADKTGIRATFDVKSVGA 240

Query: 241 YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLVLTS 300
           Y IKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLVLTS
Sbjct: 241 YTIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLVLTS 300

Query: 301 ADGRGIKITGSIGVGAGILHTENYGRLSLVKNDGRDINISGTGLSAIGMGATDMISQSSV 360
           ADGRGIKITGSIGVGAGILHTENYGRLSLVKN GRDINISGTGLSAIGMGATDMISQSSV
Sbjct: 301 ADGRGIKITGSIGVGAGILHTENYGRLSLVKNVGRDINISGTGLSAIGMGATDMISQSSV 360

Query: 361 SLRESKGQISAANADAMGFNAYNGGGAKQIIFASSI 396
           SLRESKGQISAANADAMGFNAYNGGGAKQIIFASSI
Sbjct: 361 SLRESKGQISAANADAMGFNAYNGGGAKQIIFASSI 396
```

tr Q46009 **Flagellin [Campylobacter coli]** 572 AA
align

```
 Score =  724 bits (1869), Expect = 0.0
 Identities = 385/396 (97%), Positives = 389/396 (98%), Gaps = 1/396 (0%)

Query: 1   GFRINTNVAALNAKANSDLNSRALDQSLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
           GFRINTNVAALNAKANSDLNSRALDQSLSRLSSGLRINSAAD ASGMAIADSLRSQANTL
Sbjct: 2   GFRINTNVAALNAKANSDLNSRALDQSLSRLSSGLRINSAADVASGMAIADSLRSQANTL 61

Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120
           GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAA+DGQSLKTRTMLQADINRLME
Sbjct: 62  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAEDGQSLKTRTMLQADINRLME 121

Query: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 180
           ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTR    ++ F
Sbjct: 122 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRLNRFTK-F 180

Query: 181 SSGTVGLTIKNYNGIEDFKFDSVVISTSVGTGLGALAEEINRNADKTGIRATFDVKSVGA 240
           SSGTVGLTIKNYNGIEDFKFDSVVISTSVGTGLGALAEEINRNADKTGIRATFD+KSVGA
Sbjct: 181 SSGTVGLTIKNYNGIEDFKFDSVVISTSVGTGLGALAEEINRNADKTGIRATFDLKSVGA 240

Query: 241 YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLVLTS 300
           YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLVLTS
Sbjct: 241 YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLVLTS 300

Query: 301 ADGRGIKITGSIGVGAGILHTENYGRLSLVKNDGRDINISGTGLSAIGMGATDMISQSSV 360
           ADGRGIKITGSIGVGAGILHTENYGRLSLVKNDGRDINISGTG SAIGMGATDMISQSSV
Sbjct: 301 ADGRGIKITGSIGVGAGILHTENYGRLSLVKNDGRDINISGTGFSAIGMGATDMISQSSV 360

Query: 361 SLRESKGQISAANADAMGFNAYNGGGAKQIIFASSI 396
           SLRESKGQISAANADAMGFNAYNGGGAKQIIFASSI
Sbjct: 361 SLRESKGQISAANADAMGFNAYNGGGAKQIIFASSI 396
```

sp P18245 FLAB_CAMCO **Flagellin B (Flagellin N) [flaB] [Campylobacter coli]** 572 AA
align

tr Q9RPY6 **Flagellin A [flaA] [Campylobacter jejuni]** 574 AA
align

Score = 722 bits (1863), Expect = 0.0
Identities = 379/396 (95%), Positives = 388/396 (97%), Gaps = 2/396 (0%)

```
Query: 1   GFRINTNVAALNAKANSDLNSRALDQSLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
           GFRINTNVAALNAKANSDLNSRALDQSLSRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 2   GFRINTNVAALNAKANSDLNSRALDQSLSRLSSGLRINSAADDASGMAIADSLRSQANTL 61

Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120
           GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME
Sbjct: 62  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 121

Query: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 180
           ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF
Sbjct: 122 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 181

Query: 181 SSGTVGLTIKNYNGIEDFKFDSVVISTSVGTGLGALAEEINRNADKTGIRATFDVKSVGA 240
           SSGTVGLTIKNYNGIEDFKFDSVVISTSVGTGLGALAEEINRNADKTGIRATFDVKSVGA
Sbjct: 182 SSGTVGLTIKNYNGIEDFKFDSVVISTSVGTGLGALAEEINRNADKTGIRATFDVKSVGA 241

Query: 241 YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLVLTS 300
           YAIKAGNTSQDFAINGVVIG+++Y+DGD NG LISAINAVKDTTGVQASKDENGKLVLTS
Sbjct: 242 YAIKAGNTSQDFAINGVVIGQINYNDGDNNGQLISAINAVKDTTGVQASKDENGKLVLTS 301

Query: 301 ADGRGIKITGSIGVGAGILHTENYGRLSLVKNDGRDINISGTGLSAIGMGATDMISQSSV 360
           ADGRGIKITGSIGVGAGILHTENYGRLSLVKNDGRDINISGTGLSAIGMGATDMISQSSV
Sbjct: 302 ADGRGIKITGSIGVGAGILHTENYGRLSLVKNDGRDINISGTGLSAIGMGATDMISQSSV 361

Query: 361 SLRESKGQISAANADAMGFNAYNGGGAKQIIFASSI 396
           SLRESKGQISAANADAMGFN+Y GGG  + +F  ++
Sbjct: 362 SLRESKGQISAANADAMGFNSYKGGG--KFVFTQNV 395
```

tr Q99QL6 **Flagellin A (Fragment) [flaA] [Campylobacter jejuni]** 574 AA
align

Score = 702 bits (1813), Expect = 0.0
Identities = 366/398 (91%), Positives = 385/398 (95%), Gaps = 2/398 (0%)

```
Query: 1   GFRINTNVAALNAKANSDLNSRALDQSLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
           GFRINTN AALNAKANSDLN+++LD SL+RLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 1   GFRINTNGAALNAKANSDLNAKSLDSSLARLSSGLRINSAADDASGMAIADSLRSQANTL 60

Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120
           GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LME
Sbjct: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120

Query: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 180
           ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQT+KA+IGATQSSKIGVTRFETGSQSF
Sbjct: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTVKATIGATQSSKIGVTRFETGSQSF 180

Query: 181 SSGTVGLTIKNYNGIEDFKFDSVVISTSVGTGLGALAEEINRNADKTGIRATFDVKSVGA 240
           +SG VGLTIKNYNGIEDFKFD+VVISTSVGTGLGALAEEIN+NADKTG+RAT+DVK+ GA
```

```
Sbjct: 181 TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKNADKTGVRATYDVKTTGA 240

Query: 241 YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLVLTS 300
           YAIKAG TSQDFAINGV+IGKVDY DGD NGSLISAINAVKDTTGVQASKDENGKLVLTS
Sbjct: 241 YAIKAGTTSQDFAINGVIIGKVDYKDGDNNGSLISAINAVKDTTGVQASKDENGKLVLTS 300

Query: 301 ADGRGIKITGSIGVGAGILHT--ENYGRLSLVKNDGRDINISGTGLSAIGMGATDMISQS 358
           ADGRGIKITG IGVG+GIL T  ENYGRLSLVKNDGRDIN+SGTGLSAIGMGA DMISQ+
Sbjct: 301 ADGRGIKITGDIGVGSGILSTQKENYGRLSLVKNDGRDINVSGTGLSAIGMGAADMISQA 360

Query: 359 SVSLRESKGQISAANADAMGFNAYNGGGAKQIIFASSI 396
           SVSLRESKGQISAANADAMGFN+YNGGGAKQI+ ASSI
Sbjct: 361 SVSLRESKGQISAANADAMGFNSYNGGGAKQILQASSI 398
```

tr Q99Q27 **Flagellin A (Fragment) [flaA] [Campylobacter jejuni]** 576 AA
align

```
 Score =  696 bits (1796), Expect = 0.0
 Identities = 365/400 (91%), Positives = 384/400 (95%), Gaps = 4/400 (1%)

Query: 1   GFRINTNVAALNAKANSDLNSRALDQSLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
           GFRINTN AALNAKANSDLN+++LD SL+RLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 1   GFRINTNGAALNAKANSDLNAKSLDSSLARLSSGLRINSAADDASGMAIADSLRSQANTL 60

Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120
           GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LME
Sbjct: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120

Query: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 180
           ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQT+KA+IGATQSSKIGVTRFETGSQSF
Sbjct: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTVKATIGATQSSKIGVTRFETGSQSF 180

Query: 181 SSGTVGLTIKNYNGIEDFKFDSVVISTSVGTGLGALAEEINRNADKTGIRATFDVKSVGA 240
           +SG VGLTIKNYNGIEDFKFD+VVISTSVGTGLGALAEEIN+NADKTG+RAT+DVK+ GA
Sbjct: 181 TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKNADKTGVRATYDVKTTGA 240

Query: 241 YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLVLTS 300
           YAIKAG TSQDFAINGV+IGKVDY DGD NGSLISAINAVKDTTGVQASKDENGKLVLTS
Sbjct: 241 YAIKAGTTSQDFAINGVIIGKVDYKDGDNNGSLISAINAVKDTTGVQASKDENGKLVLTS 300

Query: 301 ADGRGIKITGSIGVGAGIL--HTENYGRLSLVKNDGRDINISGTGLSAIGMGATDMISQS 358
           ADGRGIKITG IGVG+GIL    ENYGRLSLVKNDGRDIN+SGTGLSAIGMGA DMISQ+
Sbjct: 301 ADGRGIKITGDIGVGSGILSAQKENYGRLSLVKNDGRDINVSGTGLSAIGMGAADMISQA 360

Query: 359 SVSLRESKGQISAANADAMGFNAYNGGGAKQI--IFASSI 396
           SVSLRESKGQISAANADAMGFN+YNGGGAKQI  + ASSI
Sbjct: 361 SVSLRESKGQISAANADAMGFNSYNGGGAKQILQVQASSI 400
```

tr Q93NL6 **Flagellin A (Fragment) [flaA] [Campylobacter jejuni]** 557 AA
align

```
 Score =  687 bits (1774), Expect = 0.0
 Identities = 358/389 (92%), Positives = 377/389 (96%), Gaps = 2/389 (0%)
```

```
Query: 10  ALNAKANSDLNSRALDQSLSRLSSGLRINSAADDASGMAIADSLRSQANTLGQAISNGND 69
           ALNAKANSDLN+++LD SL+RLSSGLRINSAADDASGMAIADSLRSQANTLGQAISNGND
Sbjct: 1   ALNAKANSDLNAKSLDSSLARLSSGLRINSAADDASGMAIADSLRSQANTLGQAISNGND 60

Query: 70  ALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLMEELDNIANTT 129
           ALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LMEELDNIANTT
Sbjct: 61  ALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLMEELDNIANTT 120

Query: 130 SFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSFSSGTVGLTI 189
           SFNGKQLLSGGFTNQEFQIGSSSNQT+KA+IGATQSSKIGVTRFETGSQSF+SG VGLTI
Sbjct: 121 SFNGKQLLSGGFTNQEFQIGSSSNQTVKATIGATQSSKIGVTRFETGSQSFTSGVVGLTI 180

Query: 190 KNYNGIEDFKFDSVVISTSVGTGLGALAEEINRNADKTGIRATFDVKSVGAYAIKAGNTS 249
           KNYNGIEDFKFD+VVISTSVGTGLGALAEEIN+NADKTG+RAT+DVK+ GAYAIKAG TS
Sbjct: 181 KNYNGIEDFKFDNVVISTSVGTGLGALAEEINKNADKTGVRATYDVKTTGAYAIKAGTTS 240

Query: 250 QDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLVLTSADGRGIKIT 309
           QDFAINGV+IGKVDY DGD NGSLISAINAVKDTTGVQASKDENGKLVLTSADGRGIKIT
Sbjct: 241 QDFAINGVIIGKVDYKDGDNNGSLISAINAVKDTTGVQASKDENGKLVLTSADGRGIKIT 300

Query: 310 GSIGVGAGILHT--ENYGRLSLVKNDGRDINISGTGLSAIGMGATDMISQSSVSLRESKG 367
           G IGVG+GIL T  ENYGRLSLVKNDGRDIN+SGTGLSAIGMGA DMISQ+SVSLRESKG
Sbjct: 301 GDIGVGSGILSTQKENYGRLSLVKNDGRDINVSGTGLSAIGMGAADMISQASVSLRESKG 360

Query: 368 QISAANADAMGFNAYNGGGAKQIIFASSI 396
           QISAANADAMGFN+YNGGGAKQI+ ASSI
Sbjct: 361 QISAANADAMGFNSYNGGGAKQILQASSI 389
```

tr Q93NL9 **Flagellin A (Fragment) [flaA] [Campylobacter jejuni]** 557 AA
align

```
 Score =  687 bits (1773), Expect = 0.0
 Identities = 358/389 (92%), Positives = 377/389 (96%), Gaps = 2/389 (0%)

Query: 10  ALNAKANSDLNSRALDQSLSRLSSGLRINSAADDASGMAIADSLRSQANTLGQAISNGND 69
           ALNAKANSDLN+++LD SL+RLSSGLRINSAADDASGMAIADSLRSQANTLGQAISNGND
Sbjct: 1   ALNAKANSDLNAKSLDSSLARLSSGLRINSAADDASGMAIADSLRSQANTLGQAISNGND 60

Query: 70  ALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLMEELDNIANTT 129
           ALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LMEELDNIANTT
Sbjct: 61  ALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLMEELDNIANTT 120

Query: 130 SFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSFSSGTVGLTI 189
           SFNGKQLLSGGFTNQEFQIGSSSNQT+KA+IGATQSSKIGVTRFETGSQSF+SG VGLTI
Sbjct: 121 SFNGKQLLSGGFTNQEFQIGSSSNQTVKATIGATQSSKIGVTRFETGSQSFTSGIVGLTI 180

Query: 190 KNYNGIEDFKFDSVVISTSVGTGLGALAEEINRNADKTGIRATFDVKSVGAYAIKAGNTS 249
           KNYNGIEDFKFD+VVISTSVGTGLGALAEEIN+NADKTG+RAT+DVK+ GAYAIKAG TS
Sbjct: 181 KNYNGIEDFKFDNVVISTSVGTGLGALAEEINKNADKTGVRATYDVKTTGAYAIKAGTTS 240

Query: 250 QDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLVLTSADGRGIKIT 309
           QDFAINGV+IGKVDY DGD NGSLISAINAVKDTTGVQASKDENGKLVLTSADGRGIKIT
Sbjct: 241 QDFAINGVIIGKVDYKDGDNNGSLISAINAVKDTTGVQASKDENGKLVLTSADGRGIKIT 300
```

```
Query: 310 GSIGVGAGILHT--ENYGRLSLVKNDGRDINISGTGLSAIGMGATDMISQSSVSLRESKG 367
           G IGVG+GIL T  ENYGRLSLVKNDGRDIN+SGTGLSAIGMGA DMISQ+SVSLRESKG
Sbjct: 301 GDIGVGSGILFTQKENYGRLSLVKNDGRDINVSGTGLSAIGMGAADMISQASVSLRESKG 360

Query: 368 QISAANADAMGFNAYNGGGAKQIIFASSI 396
           QISAANADAMGFN+YNGGGAKQI+ ASSI
Sbjct: 361 QISAANADAMGFNSYNGGGAKQILQASSI 389
```

sp P22251 FLA2_CAMJE **Flagellin A [flaA] [Campylobacter jejuni]** 575 AA align

```
 Score =  674 bits (1738), Expect = 0.0
 Identities = 351/398 (88%), Positives = 374/398 (93%), Gaps = 4/398 (1%)

Query: 1   GFRINTNVAALNAKANSDLNSRALDQSLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
           GFRINTNVAALNAKANSDLN+++LD SLSRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 1   GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60

Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120
           GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LME
Sbjct: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120

Query: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 180
           ELDNIANTTSFNGKQLLSG FTNQEFQIG+SSNQT+KA+IGATQSSKIGVTRFETG+QSF
Sbjct: 121 ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180

Query: 181 SSGTVGLTIKNYNGIEDFKFDSVVISTSVGTGLGALAEEINRNADKTGIRATFDVKSVGA 240
           +SG VGLTIKNYNGIEDFKFD+VVISTSVGTGLGALAEEIN++ADKTG+RAT+DVK+ G
Sbjct: 181 TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240

Query: 241 YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLVLTS 300
           YAIK G TSQDFAINGV IGK++Y DGD NGSLISAINAVKDTTGVQASKDENGKLVLTS
Sbjct: 241 YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 300

Query: 301 ADGRGIKITGSIGVGAGIL--HTENYGRLSLVKNDGRDINISGTGLSAIGMGATDMISQS 358
           ADGRGIKITG IGVG+GIL    ENYGRLSLVKNDGRDINISGT LSAIGMG TDMISQS
Sbjct: 301 ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360

Query: 359 SVSLRESKGQISAANADAMGFNAYNGGGAKQIIFASSI 396
           SVSLRESKGQISA NADAMGFN+Y GGG  + +F  ++
Sbjct: 361 SVSLRESKGQISATNADAMGFNSYKGGG--KFVFTQNV 396
```

tr Q8G9F3 **Flagellin (Fragment) [flaA] [Campylobacter coli]** 575 AA align

```
 Score =  674 bits (1738), Expect = 0.0
 Identities = 352/398 (88%), Positives = 377/398 (94%), Gaps = 4/398 (1%)

Query: 1   GFRINTNVAALNAKANSDLNSRALDQSLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
           GFRINTN AALNAKANSDLNS++LDQSL+RLSSGLRINSAADDASGMAIADSLRSQA+TL
Sbjct: 1   GFRINTNGAALNAKANSDLNSKSLDQSLARLSSGLRINSAADDASGMAIADSLRSQASTL 60

Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120
```

```
            GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME
Sbjct: 61   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120

Query: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 180
            ELDNIANTTSFNGKQLLSGGFTNQEFQIG+SSNQTIKA+IGATQSSKIGVTRFETG+QSF
Sbjct: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGASSNQTIKATIGATQSSKIGVTRFETGAQSF 180

Query: 181 SSGTVGLTIKNYNGIEDFKFDSVVISTSVGTGLGALAEEINRNADKTGIRATFDVKSVGA 240
            +SG VGLTIKNYNGIEDFKFD+VVISTSVGTGLGALAEEIN++ADKTG+RAT+DVK+ G
Sbjct: 181 TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240

Query: 241 YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLVLTS 300
            YAIK G TSQDFAINGV IGK++Y DGD +GSLISAINAVKDTTGVQASKDENGKLVLTS
Sbjct: 241 YAIKEGTTSQDFAINGVTIGKIEYKDGDGDGSLISAINAVKDTTGVQASKDENGKLVLTS 300

Query: 301 ADGRGIKITGSIGVGAGIL--HTENYGRLSLVKNDGRDINISGTGLSAIGMGATDMISQS 358
            ADGRGIKITG IGVG+GIL    ENYGRLSLVKNDGRDINISGT LSAIGMG TDMISQS
Sbjct: 301 ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360

Query: 359 SVSLRESKGQISAANADAMGFNAYNGGGAKQIIFASSI 396
            SVSLRESKGQISA NADAMGFN+Y GGG  +++ +S++
Sbjct: 361 SVSLRESKGQISATNADAMGFNSYKGGG--KLVLSSAV 396
```

tr O85179 **Flagellin A [flaA] [Campylobacter jejuni]** 576 AA
align

```
 Score =  674 bits (1738), Expect = 0.0
 Identities = 351/398 (88%), Positives = 374/398 (93%), Gaps = 4/398 (1%)

Query: 1   GFRINTNVAALNAKANSDLNSRALDQSLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
            GFRINTNVAALNAKANSDLN+++LD SLSRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 2   GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 61

Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120
            GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LME
Sbjct: 62  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 121

Query: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 180
            ELDNIANTTSFNGKQLLSG FTNQEFQIG+SSNQT+KA+IGATQSSKIGVTRFETG+QSF
Sbjct: 122 ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 181

Query: 181 SSGTVGLTIKNYNGIEDFKFDSVVISTSVGTGLGALAEEINRNADKTGIRATFDVKSVGA 240
            +SG VGLTIKNYNGIEDFKFD+VVISTSVGTGLGALAEEIN++ADKTG+RAT+DVK+ G
Sbjct: 182 TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 241

Query: 241 YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLVLTS 300
            YAIK G TSQDFAINGV IGK++Y DGD NGSLISAINAVKDTTGVQASKDENGKLVLTS
Sbjct: 242 YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 301

Query: 301 ADGRGIKITGSIGVGAGIL--HTENYGRLSLVKNDGRDINISGTGLSAIGMGATDMISQS 358
            ADGRGIKITG IGVG+GIL    ENYGRLSLVKNDGRDINISGT LSAIGMG TDMISQS
Sbjct: 302 ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 361

Query: 359 SVSLRESKGQISAANADAMGFNAYNGGGAKQIIFASSI 396
            SVSLRESKGQISA NADAMGFN+Y GGG  + +F  ++
```

```
Sbjct: 362 SVSLRESKGQISATNADAMGFNSYKGGG--KFVFTQNV 397
```

tr Q9R950 **Flagellin A [flaA] [Campylobacter jejuni]** 576 AA
align

```
 Score =  672 bits (1733), Expect = 0.0
 Identities = 350/398 (87%), Positives = 374/398 (93%), Gaps = 4/398 (1%)

Query: 1   GFRINTNVAALNAKANSDLNSRALDQSLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
           GFRINTNVAALNAKANSDLN+++LD SLSRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 2   GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 61

Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120
           GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LME
Sbjct: 62  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 121

Query: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 180
           ELDNIANTTSFNGKQLLSG FTNQEFQIG+SSNQT+KA+IGATQSSKIGVTRFETG+QSF
Sbjct: 122 ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 181

Query: 181 SSGTVGLTIKNYNGIEDFKFDSVVISTSVGTGLGALAEEINRNADKTGIRATFDVKSVGA 240
           +SG VGLTIKNYNGIEDFKFD+VVISTSVGTGLGALAEEIN++ADKTG+RAT+DVK+ G
Sbjct: 182 TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 241

Query: 241 YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLVLTS 300
           YAIK G TSQ+FAINGV IGK++Y DGD NGSLISAINAVKDTTGVQASKDENGKLVLTS
Sbjct: 242 YAIKEGTTSQNFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 301

Query: 301 ADGRGIKITGSIGVGAGIL--HTENYGRLSLVKNDGRDINISGTGLSAIGMGATDMISQS 358
           ADGRGIKITG IGVG+GIL    ENYGRLSLVKNDGRDINISGT LSAIGMG TDMISQS
Sbjct: 302 ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 361

Query: 359 SVSLRESKGQISAANADAMGFNAYNGGGAKQIIFASSI 396
           SVSLRESKGQISA NADAMGFN+Y GGG  + +F  ++
Sbjct: 362 SVSLRESKGQISATNADAMGFNSYKGGG--KFVFTQNV 397
```

tr Q9RF26 **Chimeric flagellin A/B [Campylobacter jejuni]** 576 AA
align

```
 Score =  670 bits (1728), Expect = 0.0
 Identities = 349/398 (87%), Positives = 373/398 (93%), Gaps = 4/398 (1%)

Query: 1   GFRINTNVAALNAKANSDLNSRALDQSLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
           GFRINTNVAALNAKANSDLN+++LD SLSRLSSGLRINSAADDASGMAIADSLRSQA TL
Sbjct: 2   GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQAATL 61

Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120
           GQAI+NGNDA+GILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME
Sbjct: 62  GQAINNGNDAIGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 121

Query: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 180
           ELDNIANTTSFNGKQLLSG FTNQEFQIG+SSNQT+KA+IGATQSSKIGVTRFETG+QSF
Sbjct: 122 ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 181
```

```
Query: 181 SSGTVGLTIKNYNGIEDFKFDSVVISTSVGTGLGALAEEINRNADKTGIRATFDVKSVGA 240
           +SG VGLTIKNYNGIEDFKFD+VVISTSVGTGLGALAEEIN++ADKTG+RAT+DVK+ G
Sbjct: 182 TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 241

Query: 241 YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLVLTS 300
           YAIK G TSQDFAINGV IGK++Y DGD NGSLISAINAVKDTTGVQASKDENGKLVLTS
Sbjct: 242 YAIKEGTTSQDFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 301

Query: 301 ADGRGIKITGSIGVGAGIL--HTENYGRLSLVKNDGRDINISGTGLSAIGMGATDMISQS 358
           ADGRGIKITG IGVG+GIL    ENYGRLSLVKNDGRDINISGT LSAIGMG TDMISQS
Sbjct: 302 ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 361

Query: 359 SVSLRESKGQISAANADAMGFNAYNGGGAKQIIFASSI 396
           SVSLRESKGQISA NADAMGFN+Y GGG  + +F  ++
Sbjct: 362 SVSLRESKGQISATNADAMGFNSYKGGG--KFVFTQNV 397
```

tr Q9R953 **Flagellin A [flaA] [Campylobacter jejuni]** 576 AA
align

```
 Score =  669 bits (1727), Expect = 0.0
 Identities = 349/398 (87%), Positives = 373/398 (93%), Gaps = 4/398 (1%)

Query: 1   GFRINTNVAALNAKANSDLNSRALDQSLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
           GFRINTN AALNAKANSDLN+++LD SLSRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 2   GFRINTNGAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 61

Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120
           GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LME
Sbjct: 62  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 121

Query: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 180
           ELDNIANTTSFNGKQLLSG FTNQEFQIG+SSNQT+KA+IGATQSSKIGVTRFETG+QSF
Sbjct: 122 ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 181

Query: 181 SSGTVGLTIKNYNGIEDFKFDSVVISTSVGTGLGALAEEINRNADKTGIRATFDVKSVGA 240
           +SG VGLTIKNYNGIEDFKFD+VVISTSVGTGLGALAEEIN++ADKTG+RAT+DVK+ G
Sbjct: 182 TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 241

Query: 241 YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLVLTS 300
           YAIK G TSQ+FAINGV IGK++Y DGD NGSLISAINAVKDTTGVQASKDENGKLVLTS
Sbjct: 242 YAIKEGTTSQEFAINGVTIGKIEYKDGDGNGSLISAINAVKDTTGVQASKDENGKLVLTS 301

Query: 301 ADGRGIKITGSIGVGAGIL--HTENYGRLSLVKNDGRDINISGTGLSAIGMGATDMISQS 358
           ADGRGIKITG IGVG+GIL    ENYGRLSLVKNDGRDINISGT LSAIGMG TDMISQS
Sbjct: 302 ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 361

Query: 359 SVSLRESKGQISAANADAMGFNAYNGGGAKQIIFASSI 396
           SVSLRESKGQISA NADAMGFN+Y GGG  + +F  ++
Sbjct: 362 SVSLRESKGQISATNADAMGFNSYKGGG--KFVFTQNV 397
```

tr O85183 **Flagellin A [flaA] [Campylobacter jejuni]** 576 AA
align

sp P22252 FLB2_CAMJE **Flagellin B [flaB] [Campylobacter jejuni]** 575 AA align

Score = 660 bits (1703), Expect = 0.0
Identities = 344/398 (86%), Positives = 369/398 (92%), Gaps = 4/398 (1%)

```
Query: 1   GFRINTNVAALNAKANSDLNSRALDQSLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
           GFRINTN+ ALNA ANS +NS  LD+SLSRLSSGLRINSAADDASGMAIADSLRSQA TL
Sbjct: 1   GFRINTNIGALNAHANSVVNSNELDKSLSRLSSGLRINSAADDASGMAIADSLRSQAATL 60

Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120
           GQAI+NGNDA+GILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME
Sbjct: 61  GQAINNGNDAIGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120

Query: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 180
           ELDNIANTTSFNGKQLLSG FTNQEFQIG+SSNQTIKA+IGATQSSKIGVTRFETG+QSF
Sbjct: 121 ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTIKATIGATQSSKIGVTRFETGAQSF 180

Query: 181 SSGTVGLTIKNYNGIEDFKFDSVVISTSVGTGLGALAEEINRNADKTGIRATFDVKSVGA 240
           +SG VGLTIKNYNGIEDFKFD+VVISTSVGTGLGALAEEIN++ADKTG+RAT+DVK+ G
Sbjct: 181 TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 240

Query: 241 YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLVLTS 300
           YAIK G TSQDFAINGVVIG+++Y DGD NG L+SAINAVKDTTGVQASKDENGKLVLTS
Sbjct: 241 YAIKEGTTSQDFAINGVVIGQINYKDGDNNGQLVSAINAVKDTTGVQASKDENGKLVLTS 300

Query: 301 ADGRGIKITGSIGVGAGIL--HTENYGRLSLVKNDGRDINISGTGLSAIGMGATDMISQS 358
           ADGRGIKITG IGVG+GIL    ENYGRLSLVKNDGRDINISGT LSAIGMG TDMISQS
Sbjct: 301 ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360

Query: 359 SVSLRESKGQISAANADAMGFNAYNGGGAKQIIFASSI 396
           SVSLRESKGQISA NADAMGFN+Y GGG  + +F  ++
Sbjct: 361 SVSLRESKGQISATNADAMGFNSYKGGG--KFVFTQNV 396
```

tr Q9RF25 **Flagellin B [flaB] [Campylobacter jejuni]** 576 AA align

Score = 660 bits (1703), Expect = 0.0
Identities = 344/398 (86%), Positives = 369/398 (92%), Gaps = 4/398 (1%)

```
Query: 1   GFRINTNVAALNAKANSDLNSRALDQSLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
           GFRINTN+ ALNA ANS +NS  LD+SLSRLSSGLRINSAADDASGMAIADSLRSQA TL
Sbjct: 2   GFRINTNIGALNAHANSVVNSNELDKSLSRLSSGLRINSAADDASGMAIADSLRSQAATL 61

Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120
           GQAI+NGNDA+GILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME
Sbjct: 62  GQAINNGNDAIGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 121

Query: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 180
           ELDNIANTTSFNGKQLLSG FTNQEFQIG+SSNQTIKA+IGATQSSKIGVTRFETG+QSF
Sbjct: 122 ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTIKATIGATQSSKIGVTRFETGAQSF 181

Query: 181 SSGTVGLTIKNYNGIEDFKFDSVVISTSVGTGLGALAEEINRNADKTGIRATFDVKSVGA 240
           +SG VGLTIKNYNGIEDFKFD+VVISTSVGTGLGALAEEIN++ADKTG+RAT+DVK+ G
```

```
Sbjct: 182 TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 241

Query: 241 YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLVLTS 300
           YAIK G TSQDFAINGVVIG+++Y DGD NG L+SAINAVKDTTGVQASKDENGKLVLTS
Sbjct: 242 YAIKEGTTSQDFAINGVVIGQINYKDGDNNGQLVSAINAVKDTTGVQASKDENGKLVLTS 301

Query: 301 ADGRGIKITGSIGVGAGIL--HTENYGRLSLVKNDGRDINISGTGLSAIGMGATDMISQS 358
           ADGRGIKITG IGVG+GIL    ENYGRLSLVKNDGRDINISGT LSAIGMG TDMISQS
Sbjct: 302 ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 361

Query: 359 SVSLRESKGQISAANADAMGFNAYNGGGAKQIIFASSI 396
           SVSLRESKGQISA NADAMGFN+Y GGG  + +F  ++
Sbjct: 362 SVSLRESKGQISATNADAMGFNSYKGGG--KFVFTQNV 397
```

tr Q7X516 **FlaB [flaB] [Campylobacter jejuni]** 576 AA
align

```
 Score =  657 bits (1695), Expect = 0.0
 Identities = 341/398 (85%), Positives = 368/398 (91%), Gaps = 4/398 (1%)

Query: 1   GFRINTNVAALNAKANSDLNSRALDQSLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
           GFRINTN+ ALNA ANS +NS  LD+SLSRLSSGLRINSAADDASGMAIADSLRSQA TL
Sbjct: 2   GFRINTNIGALNAHANSVVNSNELDKSLSRLSSGLRINSAADDASGMAIADSLRSQAATL 61

Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120
           GQAI+NGNDA+GILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LME
Sbjct: 62  GQAINNGNDAIGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 121

Query: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 180
           ELDNIANTTSFNGKQLLSG FTNQEFQIG+SSNQT+KA+IGATQSSKIGVTRFETG+QSF
Sbjct: 122 ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 181

Query: 181 SSGTVGLTIKNYNGIEDFKFDSVVISTSVGTGLGALAEEINRNADKTGIRATFDVKSVGA 240
           +SG VGLTIKNYNGIEDFKFD+VVISTSVGTGLGALAEEIN++ADKTG+RAT+DVK+ G
Sbjct: 182 TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGV 241

Query: 241 YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLVLTS 300
           YAIK G TSQDFAINGV IG+++Y DGD NG L+SAINAVKDTTGVQASKDENGKLVLTS
Sbjct: 242 YAIKEGTTSQDFAINGVAIGQINYKDGDNNGQLVSAINAVKDTTGVQASKDENGKLVLTS 301

Query: 301 ADGRGIKITGSIGVGAGIL--HTENYGRLSLVKNDGRDINISGTGLSAIGMGATDMISQS 358
           ADGRGIKITG IGVG+GIL    ENYGRLSLVKNDGRDINISGT LSAIGMG TDMISQS
Sbjct: 302 ADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQS 361

Query: 359 SVSLRESKGQISAANADAMGFNAYNGGGAKQIIFASSI 396
           SVSLRESKGQISA NADAMGFN+Y GGG  + +F  ++
Sbjct: 362 SVSLRESKGQISATNADAMGFNSYKGGG--KFVFTQNV 397
```

tr Q6L5K6 **Flagellin (Fragment) [flaA] [Campylobacter lari]** 568 AA
align

```
 Score =  608 bits (1568), Expect = e-173
 Identities = 321/396 (81%), Positives = 351/396 (88%), Gaps = 2/396 (0%)
```

```
Query: 1   GFRINTNVAALNAKANSDLNSRALDQSLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
           GFRINTNVA+LNA+AN++LNSRALD SLSRLSSGLRINSAADDASGMAIADSLRSQA+TL
Sbjct: 1   GFRINTNVASLNAQANANLNSRALDTSLSRLSSGLRINSAADDASGMAIADSLRSQASTL 60

Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120
           GQAI+NGNDALGILQTADKAMDEQLKILDTIK KATQAAQDGQS KTR MLQADINRLME
Sbjct: 61  GQAINNGNDALGILQTADKAMDEQLKILDTIKVKATQAAQDGQSTKTRNMLQADINRLME 120

Query: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 180
           ELDNIANTTSFNGKQLLSGGFTNQEFQIGS SNQ+IKA+IGATQSSKIGVTRFETGS S
Sbjct: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSQSNQSIKATIGATQSSKIGVTRFETGSMSN 180

Query: 181 SSGTVGLTIKNYNGIEDFKFDSVVISTSVGTGLGALAEEINRNADKTGIRATFDVKSVGA 240
           +SG   LTIKNYNGI+DFKF  VVISTSVGTG+GALAEEINR +D TG+RA F V++ G
Sbjct: 181 TSGIAQLTIKNYNGIDDFKFQPVVISTSVGTGMGALAEEINRVSDVTGVRANFLVETTGV 240

Query: 241 YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLVLTS 300
            AIKA  TSQDF+INGV IG+V+Y DGDENG+LISAIN+VKDTTGV+ASKD NG+LVL S
Sbjct: 241 GAIKADKTSQDFSINGVRIGEVEYKDGDENGALISAINSVKDTTGVEASKDANGRLVLNS 300

Query: 301 ADGRGIKITGSIGVGAGILHT--ENYGRLSLVKNDGRDINISGTGLSAIGMGATDMISQS 358
            DGRGIKI GS+G+GAG+L    ENYGRLSLVKNDG+DI ISGT LS IGMGA DMISQ+
Sbjct: 301 RDGRGIKIEGSMGMGAGVLKADYENYGRLSLVKNDGKDIAISGTNLSTIGMGAADMISQA 360

Query: 359 SVSLRESKGQISAANADAMGFNAYNGGGAKQIIFAS 394
           S+SLRESKG I    ADAMGFNAY GGG   + F+S
Sbjct: 361 SISLRESKGNIDTNVADAMGFNAYKGGGKMIVTFSS 396
```

tr Q6L5K7 **Flagellin (Fragment) [flaA] [Campylobacter lari]** 563 AA
align

```
 Score =  606 bits (1563), Expect = e-172
 Identities = 319/396 (80%), Positives = 352/396 (88%), Gaps = 2/396 (0%)

Query: 1   GFRINTNVAALNAKANSDLNSRALDQSLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
           GFRINTNVA+LNA+ N++LNSRALD SLSRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 1   GFRINTNVASLNAQNNANLNSRALDTSLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60

Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120
           GQAI+NGNDALGILQTADKAMDEQLKILDTIK KATQAAQDGQS KTR MLQADINRLME
Sbjct: 61  GQAINNGNDALGILQTADKAMDEQLKILDTIKVKATQAAQDGQSTKTRNMLQADINRLME 120

Query: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 180
           ELDNIANTTSFNGKQLLSGGFTNQ FQIG+ SNQTI+ASIGATQSSKIGVTRFETGS S
Sbjct: 121 ELDNIANTTSFNGKQLLSGGFTNQSFQIGAQSNQTIQASIGATQSSKIGVTRFETGSMSH 180

Query: 181 SSGTVGLTIKNYNGIEDFKFDSVVISTSVGTGLGALAEEINRNADKTGIRATFDVKSVGA 240
           SSG   LTIKNYNGI+DFKF  VVIS+SVGTG+GALAEEINR AD TG+RA F V++ GA
Sbjct: 181 SSGVAQLTIKNYNGIDDFKFQPVVISSSVGTGIGALAEEINRVADITGVRANFLVQTTGA 240

Query: 241 YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLVLTS 300
            +IKA  TSQDF+INGV +G+V+Y DGDENG+LISAIN+VKDTTGV+ASKD NG+LVL S
Sbjct: 241 GSIKADKTSQDFSINGVKVGEVEYKDGDENGALISAINSVKDTTGVEASKDANGRLVLNS 300
```

```
Query: 301 ADGRGIKITGSIGVGAGILHTE--NYGRLSLVKNDGRDINISGTGLSAIGMGATDMISQS 358
           DGRGI+ITGSIG G+GI+  +  N+GRLSLVKNDG+DI ISG+GLSAIGMGA DMISQ+
Sbjct: 301 RDGRGIEITGSIGFGSGIMKDDYKNFGRLSLVKNDGKDILISGSGLSAIGMGAADMISQA 360

Query: 359 SVSLRESKGQISAANADAMGFNAYNGGGAKQIIFAS 394
           S+SLRESKG I    ADAMGFNAY GGG   + FA+
Sbjct: 361 SISLRESKGNIDTNVADAMGFNAYKGGGKMIVTFAN 396
```

tr Q6L5K1 **Flagellin (Fragment) [flaA] [Campylobacter lari]** 568 AA
align

```
 Score =  606 bits (1562), Expect = e-172
 Identities = 320/396 (80%), Positives = 350/396 (87%), Gaps = 2/396 (0%)

Query: 1   GFRINTNVAALNAKANSDLNSRALDQSLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
           GFRINTNVA+LNA+AN++LNSRALD SLSRLSSGLRINSAADDASGMAIADSLRSQA+TL
Sbjct: 1   GFRINTNVASLNAQANANLNSRALDTSLSRLSSGLRINSAADDASGMAIADSLRSQASTL 60

Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120
           GQAI+NGNDALGILQTADKAMDEQLKILDTIK KATQAAQDGQS KTR MLQADINRLME
Sbjct: 61  GQAINNGNDALGILQTADKAMDEQLKILDTIKVKATQAAQDGQSTKTRNMLQADINRLME 120

Query: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 180
           ELDNIANTT+FNGKQLLSGGFTNQEFQIGS SNQ+IKA+IGATQSSKIGVTRFETGS S
Sbjct: 121 ELDNIANTTAFNGKQLLSGGFTNQEFQIGSQSNQSIKATIGATQSSKIGVTRFETGSMSK 180

Query: 181 SSGTVGLTIKNYNGIEDFKFDSVVISTSVGTGLGALAEEINRNADKTGIRATFDVKSVGA 240
            SG   LTIKNYNGI+DFKF  VVISTSVGTG+GALAEEINR AD TG+RA F V++ G
Sbjct: 181 DSGIAQLTIKNYNGIDDFKFQPVVISTSVGTGMGALAEEINRVADVTGVRANFLVETTGV 240

Query: 241 YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLVLTS 300
            AIKA  TSQDF+INGV IG+V+Y DGDENG+LISAIN+VKDTTGV+ASKD NG+LVL S
Sbjct: 241 GAIKADKTSQDFSINGVRIGEVEYKDGDENGALISAINSVKDTTGVEASKDANGRLVLNS 300

Query: 301 ADGRGIKITGSIGVGAGILHT--ENYGRLSLVKNDGRDINISGTGLSAIGMGATDMISQS 358
           DGRGIKI GS+G+GAG+L    ENYGRLSLVKNDG+DI ISG+ LS IGMGAT MISQ+
Sbjct: 301 RDGRGIKIEGSMGMGAGVLKADYENYGRLSLVKNDGKDIAISGSNLSTIGMGATQMISQA 360

Query: 359 SVSLRESKGQISAANADAMGFNAYNGGGAKQIIFAS 394
           S+SLRESKG I    ADAMGFNAY GGG   + F+S
Sbjct: 361 SISLRESKGNIDTNVADAMGFNAYKGGGKMIVTFSS 396
```

tr Q6L5J8 **Flagellin (Fragment) [flaA] [Campylobacter lari]** 568 AA
align

```
 Score =  604 bits (1558), Expect = e-172
 Identities = 319/396 (80%), Positives = 350/396 (87%), Gaps = 2/396 (0%)

Query: 1   GFRINTNVAALNAKANSDLNSRALDQSLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
           GFRINTNVA+LNA+AN++LNSRALD SLSRLSSGLRINSAADDASGMAIADSLRSQA+TL
Sbjct: 1   GFRINTNVASLNAQANANLNSRALDTSLSRLSSGLRINSAADDASGMAIADSLRSQASTL 60

Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120
```

```
           GQAI+NGNDALGILQTADKAMDEQLKILDTIK KATQAAQDGQS KTR MLQADINRLME
Sbjct: 61  GQAINNGNDALGILQTADKAMDEQLKILDTIKVKATQAAQDGQSTKTRNMLQADINRLME 120

Query: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 180
           ELDNIANTT+FNGKQLLSGGFTNQEFQIG+ SNQ+IKA+IGATQSSKIGVTRFETGS S
Sbjct: 121 ELDNIANTTAFNGKQLLSGGFTNQEFQIGAQSNQSIKATIGATQSSKIGVTRFETGSMSN 180

Query: 181 SSGTVGLTIKNYNGIEDFKFDSVVISTSVGTGLGALAEEINRNADKTGIRATFDVKSVGA 240
           +SG   LTIKNYNGI+DFKF  VVISTSVGTG+GALAEEINR AD TG+RA F V++ G
Sbjct: 181 TSGIAQLTIKNYNGIDDFKFQPVVISTSVGTGMGALAEEINRVADVTGVRANFLVETTGV 240

Query: 241 YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLVLTS 300
            AIKA  TSQDF INGV IG+V+Y DGDENG+LISAIN+VKDTTGV+ASKD NG+LVL S
Sbjct: 241 GAIKADKTSQDFTINGVRIGEVEYKDGDENGALISAINSVKDTTGVEASKDANGRLVLNS 300

Query: 301 ADGRGIKITGSIGVGAGILHT--ENYGRLSLVKNDGRDINISGTGLSAIGMGATDMISQS 358
            DGRGIKI GS+G+GAG+L    ENYGRLSLVKNDG+DI ISG+ LS IGMGA DMISQ+
Sbjct: 301 RDGRGIKIEGSMGMGAGVLKADYENYGRLSLVKNDGKDIAISGSNLSTIGMGAGDMISQA 360

Query: 359 SVSLRESKGQISAANADAMGFNAYNGGGAKQIIFAS 394
           S+SLRESKG I    ADAMGFNAY GGG   + F+S
Sbjct: 361 SISLRESKGNIDTNVADAMGFNAYKGGGKMIVTFSS 396
```

tr Q6L5K8 **Flagellin (Fragment) [flaA] [Campylobacter lari]** 567 AA
align

```
 Score =  604 bits (1557), Expect = e-171
 Identities = 319/396 (80%), Positives = 351/396 (88%), Gaps = 2/396 (0%)

Query: 1   GFRINTNVAALNAKANSDLNSRALDQSLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
           GFRINTNVA+LNA+ N++LNSRALD SLSRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 1   GFRINTNVASLNAQNNANLNSRALDSSLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60

Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120
           GQAI+NGNDALGILQTADKAMDEQLKILDTIK KATQAAQDGQS KTR MLQADINRLME
Sbjct: 61  GQAINNGNDALGILQTADKAMDEQLKILDTIKVKATQAAQDGQSTKTRNMLQADINRLME 120

Query: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 180
           ELDNIANTT+FNGKQLLSGGFTNQ FQIG+ SNQTI+ASIGATQSSKIGVTRFETGS S
Sbjct: 121 ELDNIANTTAFNGKQLLSGGFTNQSFQIGAQSNQTIQASIGATQSSKIGVTRFETGSMSH 180

Query: 181 SSGTVGLTIKNYNGIEDFKFDSVVISTSVGTGLGALAEEINRNADKTGIRATFDVKSVGA 240
           SSG   LTIKNYNGI+DFKF  VVIS+SVGTG+GALAEEINR AD TG+RA F V++ GA
Sbjct: 181 SSGVAQLTIKNYNGIDDFKFQPVVISSSVGTGMGALAEEINRVADVTGVRANFLVQTTGA 240

Query: 241 YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLVLTS 300
            +IKA  TSQDF INGV IG+V+Y DGDENG+LISAIN+VKDTTGV+ASKD NG+LVL S
Sbjct: 241 GSIKADKTSQDFTINGVKIGEVEYKDGDENGALISAINSVKDTTGVEASKDANGRLVLNS 300

Query: 301 ADGRGIKITGSIGVGAGILHTE--NYGRLSLVKNDGRDINISGTGLSAIGMGATDMISQS 358
            DGRGI+ITG++GVG+G+L  +  N+GRLSLVKNDG+DI ISG+GLS IGMGA DMISQ+
Sbjct: 301 RDGRGIEITGNMGVGSGVLKDDYKNFGRLSLVKNDGKDILISGSGLSFIGMGAGDMISQA 360

Query: 359 SVSLRESKGQISAANADAMGFNAYNGGGAKQIIFAS 394
           SVSLRESKG I    ADAMGFNAY GGG   I F+S
```

```
Sbjct: 361 SVSLRESKGNIDTHVADAMGFNAYKGGGKMVITFSS 396
```

tr Q6L5K2 **Flagellin (Fragment) [flaA] [Campylobacter lari]** 567 AA
align

```
 Score =  603 bits (1555), Expect = e-171
 Identities = 317/396 (80%), Positives = 351/396 (88%), Gaps = 2/396 (0%)

Query: 1   GFRINTNVAALNAKANSDLNSRALDQSLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
           GFRINTNVA+LNA+ N++LNSRALD SLSRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 1   GFRINTNVASLNAQNNANLNSRALDSSLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60

Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120
           GQAI+NGNDALGILQTADKAMDEQLKILDTIK KATQAAQDGQS KTR MLQADINRLME
Sbjct: 61  GQAINNGNDALGILQTADKAMDEQLKILDTIKVKATQAAQDGQSTKTRNMLQADINRLME 120

Query: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 180
           ELDNIANTT+FNGKQLLSGGFTNQ FQIG+ SNQTI+ASIGATQSSKIGVTRFETGS S
Sbjct: 121 ELDNIANTTAFNGKQLLSGGFTNQSFQIGAQSNQTIQASIGATQSSKIGVTRFETGSMSH 180

Query: 181 SSGTVGLTIKNYNGIEDFKFDSVVISTSVGTGLGALAEEINRNADKTGIRATFDVKSVGA 240
           SSG   LTIKNYNGI+DFKF  VVIS+SVGTG+GALAEEINR AD TG+RA F V++ GA
Sbjct: 181 SSGVAQLTIKNYNGIDDFKFQPVVISSSVGTGMGALAEEINRVADVTGVRANFLVQTTGA 240

Query: 241 YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLVLTS 300
            +IKA  TSQDF INGV IG+V+Y DGDENG+LISAIN+VKDTTGV+ASKD NG+LVL S
Sbjct: 241 GSIKADKTSQDFTINGVKIGEVEYKDGDENGALISAINSVKDTTGVEASKDANGRLVLNS 300

Query: 301 ADGRGIKITGSIGVGAGILHTE--NYGRLSLVKNDGRDINISGTGLSAIGMGATDMISQS 358
            DGRGI+ITG++GVG+G+L  +  N+GRLSLVKNDG+DI ISG+GLS IGMGA DMISQ+
Sbjct: 301 RDGRGIEITGNMGVGSGVLKDDYKNFGRLSLVKNDGKDILISGSGLSFIGMGAGDMISQA 360

Query: 359 SVSLRESKGQISAANADAMGFNAYNGGGAKQIIFAS 394
           S+SLRESKG I    ADAMGFNAY GGG   + F+S
Sbjct: 361 SISLRESKGNIDTHIADAMGFNAYKGGGKMVVTFSS 396
```

tr Q6L5K9 **Flagellin (Fragment) [flaA] [Campylobacter lari]** 567 AA
align

```
 Score =  602 bits (1553), Expect = e-171
 Identities = 318/396 (80%), Positives = 350/396 (88%), Gaps = 2/396 (0%)

Query: 1   GFRINTNVAALNAKANSDLNSRALDQSLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
           GFRINTNVA+LNA+ N++LNSRALD SLSRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 1   GFRINTNVASLNAQNNANLNSRALDSSLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60

Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120
           GQAI+NGNDALGILQTADKAMDEQLKILDTIK KATQAAQDGQS KTR MLQADINRLME
Sbjct: 61  GQAINNGNDALGILQTADKAMDEQLKILDTIKVKATQAAQDGQSTKTRNMLQADINRLME 120

Query: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 180
           ELDNIANTT+FNGKQLLSGGFTNQ FQIG+ SNQTI+A IGATQSSKIGVTRFETGS S
Sbjct: 121 ELDNIANTTAFNGKQLLSGGFTNQSFQIGAQSNQTIQAGIGATQSSKIGVTRFETGSMSH 180
```

==========

Welcome to the SIB BLAST Network Service

If results of this search are reported or published, please mention that the computation was performed at the SIB using the BLAST network service. The SIB BLAST network service uses a server developed at SIB and the NCBI BLAST 2 software.

In case of problems, please read the online BLAST help.
If your question is not covered, please contact <helpdesk@expasy.org>.

NCBI BLAST program reference [PMID:9254694]:
Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W., Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25:3389-3402(1997).

==========

Query length: 420 AA (of which 5% low-complexity regions filtered out)
Date run: 2004-09-02 16:29:13 UTC+0100 on sib-gm1.unil.ch
Program: NCBI BLASTP 1.5.4-Paracel [2003-06-05]
Database: EXPASY/UniProt
1,544,870 sequences; 494,584,931 total letters

Taxonomic view | NiceBlast view | Printable view

List of potentially matching sequences

Send selected sequences to Clustal W (multiple alignment) Submit Query

Select up to...

☐ Include query sequence

	Db	AC	Description	Score	E-value
☐	sp	P27053	FLAA_CAMCO Flagellin A [flaA] [Campylobacter coli]	750	0.0
☐	tr	Q84IB9	Flagellin (Fragment) [flaA] [Campylobacter jejuni]	736	0.0
☐	tr	Q46009	Flagellin [Campylobacter coli]	724	0.0
☐	sp	P18245	FLAB_CAMCO Flagellin B (Flagellin N) [flaB] [Campyloba...	723	0.0
☐	tr	Q9RPY6	Flagellin A [flaA] [Campylobacter jejuni]	722	0.0
☐	tr	Q99QL6	Flagellin A (Fragment) [flaA] [Campylobacter jejuni]	702	0.0
☐	tr	Q99Q27	Flagellin A (Fragment) [flaA] [Campylobacter jejuni]	696	0.0
☐	tr	Q93NL6	Flagellin A (Fragment) [flaA] [Campylobacter jejuni]	687	0.0
☐	tr	Q93NL9	Flagellin A (Fragment) [flaA] [Campylobacter jejuni]	687	0.0
☐	sp	P22251	FLA2_CAMJE Flagellin A [flaA] [Campylobacter jejuni]	674	0.0

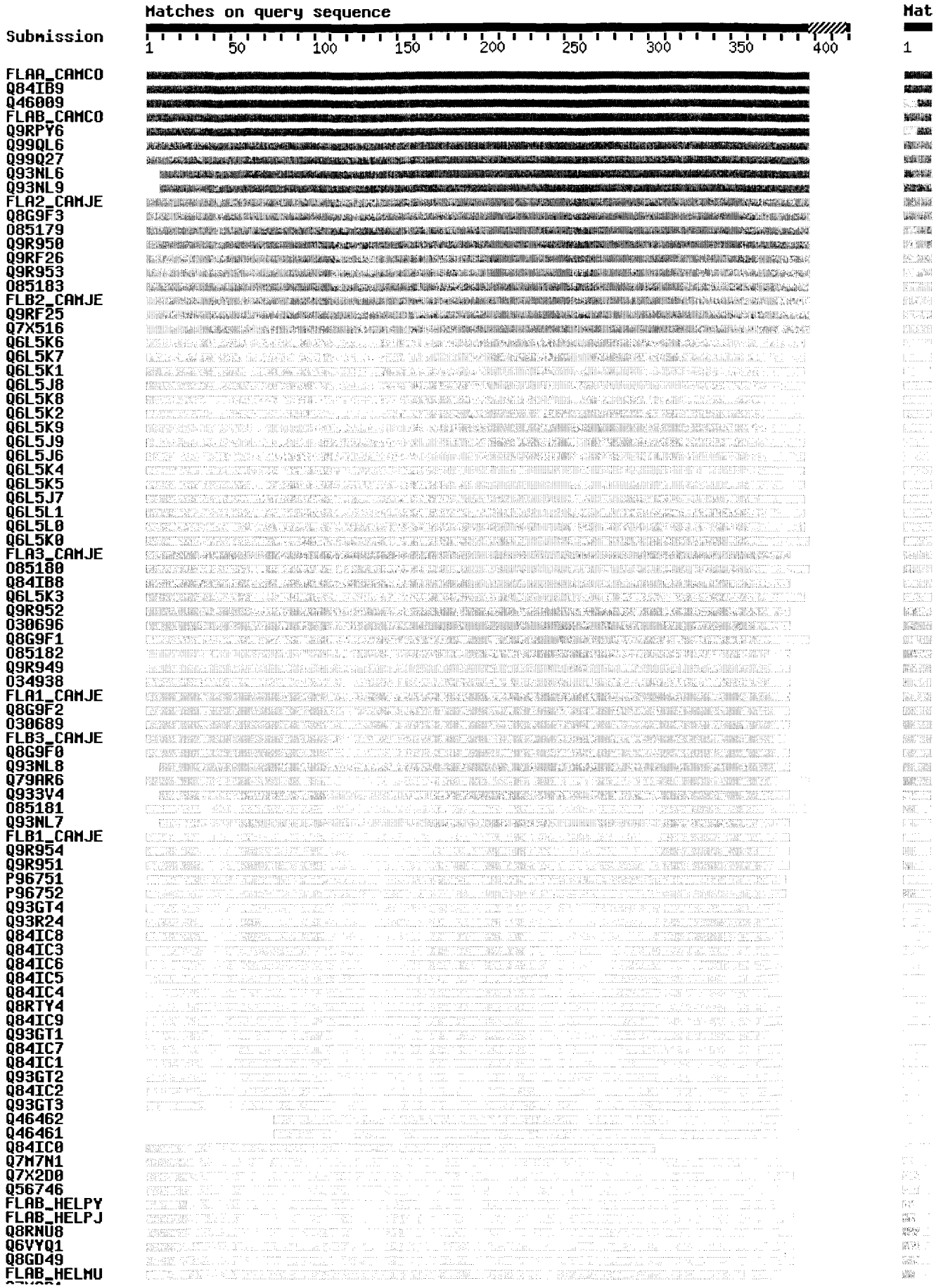
tr Q8G9F3	Flagellin (Fragment) [flaA] [Campylobacter coli]	674	0.0
tr O85179	Flagellin A [flaA] [Campylobacter jejuni]	674	0.0
tr Q9R950	Flagellin A [flaA] [Campylobacter jejuni]	672	0.0
tr Q9RF26	Chimeric flagellin A/B [Campylobacter jejuni]	670	0.0
tr Q9R953	Flagellin A [flaA] [Campylobacter jejuni]	669	0.0
tr O85183	Flagellin A [flaA] [Campylobacter jejuni]	667	0.0
sp P22252	FLB2_CAMJE Flagellin B [flaB] [Campylobacter jejuni]	660	0.0
tr Q9RF25	Flagellin B [flaB] [Campylobacter jejuni]	660	0.0
tr Q7X516	FlaB [flaB] [Campylobacter jejuni]	657	0.0
tr Q6L5K6	Flagellin (Fragment) [flaA] [Campylobacter lari]	608	e-173
tr Q6L5K7	Flagellin (Fragment) [flaA] [Campylobacter lari]	606	e-172
tr Q6L5K1	Flagellin (Fragment) [flaA] [Campylobacter lari]	606	e-172
tr Q6L5J8	Flagellin (Fragment) [flaA] [Campylobacter lari]	604	e-172
tr Q6L5K8	Flagellin (Fragment) [flaA] [Campylobacter lari]	604	e-171
tr Q6L5K2	Flagellin (Fragment) [flaA] [Campylobacter lari]	603	e-171
tr Q6L5K9	Flagellin (Fragment) [flaA] [Campylobacter lari]	602	e-171
tr Q6L5J9	Flagellin (Fragment) [flaA] [Campylobacter lari]	602	e-171
tr Q6L5J6	Flagellin (Fragment) [flaA] [Campylobacter lari]	600	e-170
tr Q6L5K4	Flagellin (Fragment) [flaA] [Campylobacter lari]	600	e-170
tr Q6L5K5	Flagellin (Fragment) [flaA] [Campylobacter lari]	599	e-170
tr Q6L5J7	Flagellin (Fragment) [flaA] [Campylobacter lari]	599	e-170
tr Q6L5L1	Flagellin (Fragment) [flaA] [Campylobacter lari]	598	e-170
tr Q6L5L0	Flagellin (Fragment) [flaA] [Campylobacter lari]	598	e-170
tr Q6L5K0	Flagellin (Fragment) [flaA] [Campylobacter lari]	598	e-170
sp Q46113	FLA3_CAMJE Flagellin A [flaA] [Campylobacter jejuni]	597	e-169
tr O85180	Flagellin A [flaA] [Campylobacter jejuni]	590	e-167
tr Q84IB8	Flagellin (Fragment) [flaA] [Campylobacter jejuni]	590	e-167
tr Q6L5K3	Flagellin (Fragment) [flaA] [Campylobacter lari]	590	e-167
tr Q9R952	Flagellin A [flaA] [Campylobacter jejuni]	589	e-167
tr O30696	Flagellin A [flaA] [Campylobacter jejuni]	588	e-167
tr Q8G9F1	Flagellin (Fragment) [flaA] [Campylobacter coli]	588	e-167
tr O85182	Flagellin A [flaA] [Campylobacter jejuni]	586	e-166
tr Q9R949	Flagellin A [flaA] [Campylobacter jejuni]	586	e-166
tr O34938	Flagellin A [flaA] [Campylobacter jejuni]	585	e-166
sp P56963	FLA1_CAMJE Flagellin A [flaA] [Campylobacter jejuni]	585	e-166
tr Q8G9F2	Flagellin (Fragment) [flaA] [Campylobacter jejuni]	584	e-166
tr O30689	Flagellin A [flaA] [Campylobacter jejuni]	583	e-165
sp Q46114	FLB3_CAMJE Flagellin B [flaB] [Campylobacter jejuni]	581	e-165
tr Q8G9F0	Flagellin (Fragment) [flaA] [Campylobacter jejuni]	578	e-164
tr Q93NL8	Flagellin A (Fragment) [flaA] [Campylobacter jejuni]	572	e-162
tr Q79AR6	Flagellin [flaA] [Campylobacter jejuni]	572	e-162
tr Q933V4	Flagellin A (Fragment) [flaA] [Campylobacter jejuni]	570	e-161
tr O85181	Flagellin B [flaB] [Campylobacter jejuni]	570	e-161
tr Q93NL7	Flagellin A (Fragment) [flaA] [Campylobacter jejuni]	569	e-161
sp P56964	FLB1_CAMJE Flagellin B [flaB] [Campylobacter jejuni]	566	e-160

tr Q9R954	Flagellin B [flaB] [Campylobacter jejuni]	565	e-160
tr Q9R951	Flagellin B [flaB] [Campylobacter jejuni]	564	e-160
tr P96751	Flagellin (Fragment) [flaA] [Campylobacter sp]	561	e-159
tr P96752	Flagellin [flaB] [Campylobacter sp]	559	e-158
tr Q93GT4	Flagellin (Fragment) [flaA] [Campylobacter lari]	489	e-137
tr Q93R24	Flagellin (Fragment) [flaA] [Campylobacter lari]	488	e-137
tr Q84IC8	Flagellin (Fragment) [flaA] [Campylobacter lari]	483	e-135
tr Q84IC3	Flagellin (Fragment) [flaA] [Campylobacter lari]	482	e-135
tr Q84IC6	Flagellin (Fragment) [flaA] [Campylobacter lari]	481	e-135
tr Q84IC5	Flagellin (Fragment) [flaA] [Campylobacter lari]	481	e-135
tr Q84IC4	Flagellin (Fragment) [flaA] [Campylobacter lari]	481	e-135
tr Q8RTY4	Flagellin (Fragment) [flaA] [Campylobacter lari]	479	e-134
tr Q84IC9	Flagellin (Fragment) [flaA] [Campylobacter lari]	479	e-134
tr Q93GT1	Flagellin (Fragment) [flaA] [Campylobacter lari]	478	e-134
tr Q84IC7	Flagellin (Fragment) [flaA] [Campylobacter lari]	478	e-133
tr Q84IC1	Flagellin (Fragment) [flaA] [Campylobacter lari]	473	e-132
tr Q93GT2	Flagellin (Fragment) [flaA] [Campylobacter lari]	473	e-132
tr Q84IC2	Flagellin (Fragment) [flaA] [Campylobacter lari]	471	e-131
tr Q93GT3	Flagellin (Fragment) [flaA] [Campylobacter lari]	463	e-129
tr Q46462	Flagellin (Fragment) [fla2] [Campylobacter upsaliensis]	453	e-126
tr Q46461	Flagellin (Fragment) [fla1] [Campylobacter upsaliensis]	444	e-123
tr Q84IC0	Flagellin (Fragment) [flaA] [Campylobacter lari]	424	e-117
tr Q7M7N1	FLAGELLIN B [FLAB] [Wolinella succinogenes]	383	e-105
tr Q7X2D0	Flagellin B [flaB] [Helicobacter pylori (Campylobacter...	380	e-104
tr Q56746	Flagellin [flag] [Wolinella succinogenes]	379	e-104
sp Q07911	FLAB_HELPY Flagellin B (Flagellin N) [flaB] [Helicobac...	376	e-103
sp Q9ZMV8	FLAB_HELPJ Flagellin B (Flagellin N) [flaB] [Helicobac...	376	e-103
tr Q8RNU8	Flagellin B subunit [flaB] [Helicobacter pylori (Campy...	376	e-103
tr Q6VYQ1	Flagellin B [flaB] [Helicobacter pylori (Campylobacter...	376	e-103
tr Q8GD49	Flagellin [flaB] [Helicobacter pylori (Campylobacter p...	375	e-103
sp Q07910	FLAB_HELMU Flagellin B (Flagellin N) [flaB] [Helicobac...	368	e-100
tr Q7X2D1	Flagellin A [flaA] [Helicobacter pylori (Campylobacter...	365	e-100
tr Q9XB37	Flagellin B [flaB] [Helicobacter felis]	365	e-100
tr Q7TTM9	Major flagellin subunit FlaA_1 (Major flagellin subuni...	363	3e-99
sp Q03843	FLAA_HELPY Flagellin A [flaA] [Helicobacter pylori (Ca...	361	1e-98
sp Q9XB38	FLAA_HELFE Flagellin A [flaA] [Helicobacter felis]	358	1e-97
tr Q6VYQ2	Flagellin A [flaA] [Helicobacter pylori (Campylobacter...	358	1e-97
tr Q7VF81	Minor flagellin subunit FlaB [flaB] [Helicobacter hepa...	356	5e-97
sp P50612	FLAA_HELMU Flagellin A [flaA] [Helicobacter mustelae]	345	9e-94
tr Q8VN93	Flagellin B (Fragment) [flaB] [Helicobacter pylori (Ca...	335	1e-90
tr Q8VN92	Flagellin B (Fragment) [flaB] [Helicobacter pylori (Ca...	334	2e-90
tr Q93NM0	Flagellin A (Fragment) [flaA] [Campylobacter jejuni]	332	8e-90
tr Q93NM1	Flagellin A (Fragment) [flaA] [Campylobacter jejuni]	332	1e-89
tr Q8VN91	Flagellin A (Fragment) [flaA] [Helicobacter pylori (Ca...	330	2e-89
tr Q8VN90	Flagellin A (Fragment) [flaA] [Helicobacter pylori (Ca...	330	2e-89

Graphical overview of the alignments

Click here to resubmit your query after masking regions matching PROSITE profiles or Pfam HMMs

(? Help) (use ScanProsite for more details about PROSITE matches)


Matches on query sequence
Mat
Submission
1
50
100
150
200
250
300
350
400
FLAA_CAMCO
Q84IB9
Q46009
FLAB_CAMCO
Q9RPY6
Q99QL6
Q99Q27
Q93NL6
Q93NL9
FLA2_CAMJE
Q8G9F3
O85179
Q9R950
Q9RF26
Q9R953
O85183
FLB2_CAMJE
Q9RF25
Q7X516
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Q6L5K7
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Q6L5K9
Q6L5J9
Q6L5J6
Q6L5K4
Q6L5K5
Q6L5J7
Q6L5L1
Q6L5L0
Q6L5K0
FLA3_CAMJE
O85180
Q84IB8
Q6L5K3
Q9R952
O30696
Q8G9F1
O85182
Q9R949
O34938
FLA1_CAMJE
Q8G9F2
O30689
FLB3_CAMJE
Q8G9F0
Q93NL8
Q79AR6
Q933V4
O85181
Q93NL7
FLB1_CAMJE
Q9R954
Q9R951
P96751
P96752
Q93GT4
Q93R24
Q84IC8
Q84IC3
Q84IC6
Q84IC5
Q84IC4
Q8RTY4
Q84IC9
Q93GT1
Q84IC7
Q84IC1
Q93GT2
Q84IC2
Q93GT3
Q46462
Q46461
Q84IC0
Q7M7N1
Q7X2D0
Q56746
FLAB_HELPY
FLAB_HELPJ
Q8RNU8
Q6VYQ1
Q8GD49
FLAB_HELMU

Alignments

sp P27053 FLAA_CAMCO **Flagellin A [flaA] [Campylobacter coli]** 572 AA align

Score = 750 bits (1937), Expect = 0.0
Identities = 396/396 (100%), Positives = 396/396 (100%)

```
Query: 1   GFRINTNVAALNAKANSDLNSRALDQSLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
           GFRINTNVAALNAKANSDLNSRALDQSLSRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 1   GFRINTNVAALNAKANSDLNSRALDQSLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60

Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120
           GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME
Sbjct: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120

Query: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 180
           ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF
Sbjct: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 180

Query: 181 SSGTVGLTIKNYNGIEDFKFDSVVISTSVGTGLGALAEEINRNADKTGIRATFDVKSVGA 240
           SSGTVGLTIKNYNGIEDFKFDSVVISTSVGTGLGALAEEINRNADKTGIRATFDVKSVGA
Sbjct: 181 SSGTVGLTIKNYNGIEDFKFDSVVISTSVGTGLGALAEEINRNADKTGIRATFDVKSVGA 240

Query: 241 YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLVLTS 300
           YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLVLTS
Sbjct: 241 YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLVLTS 300

Query: 301 ADGRGIKITGSIGVGAGILHTENYGRLSLVKNDGRDINISGTGLSAIGMGATDMISQSSV 360
           ADGRGIKITGSIGVGAGILHTENYGRLSLVKNDGRDINISGTGLSAIGMGATDMISQSSV
Sbjct: 301 ADGRGIKITGSIGVGAGILHTENYGRLSLVKNDGRDINISGTGLSAIGMGATDMISQSSV 360

Query: 361 SLRESKGQISAANADAMGFNAYNGGGAKQIIFASSI 396
           SLRESKGQISAANADAMGFNAYNGGGAKQIIFASSI
Sbjct: 361 SLRESKGQISAANADAMGFNAYNGGGAKQIIFASSI 396
```

tr Q84IB9 **Flagellin (Fragment) [flaA] [Campylobacter jejuni]** 572 AA align

Score = 736 bits (1901), Expect = 0.0
Identities = 389/396 (98%), Positives = 392/396 (98%)

```
Query: 1   GFRINTNVAALNAKANSDLNSRALDQSLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
           GFRINTN AALNAKANSDLNSRALDQSLSRLSSGLRINSAADDASGMAIADSLRSQANT+
Sbjct: 1   GFRINTNGAALNAKANSDLNSRALDQSLSRLSSGLRINSAADDASGMAIADSLRSQANTM 60

Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120
           GQAISNG+DALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME
Sbjct: 61  GQAISNGDDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120

Query: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 180
           ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF
Sbjct: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 180
```

```
Query: 181 SSGTVGLTIKNYNGIEDFKFDSVVISTSVGTGLGALAEEINRNADKTGIRATFDVKSVGA 240
           SSGTVGLTIKNYNGIEDFKF +VVISTSVGTGLGALAEEINRNADKTGIRATFDVKSVGA
Sbjct: 181 SSGTVGLTIKNYNGIEDFKFQNVVISTSVGTGLGALAEEINRNADKTGIRATFDVKSVGA 240

Query: 241 YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLVLTS 300
           Y IKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLVLTS
Sbjct: 241 YTIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLVLTS 300

Query: 301 ADGRGIKITGSIGVGAGILHTENYGRLSLVKNDGRDINISGTGLSAIGMGATDMISQSSV 360
           ADGRGIKITGSIGVGAGILHTENYGRLSLVKN GRDINISGTGLSAIGMGATDMISQSSV
Sbjct: 301 ADGRGIKITGSIGVGAGILHTENYGRLSLVKNVGRDINISGTGLSAIGMGATDMISQSSV 360

Query: 361 SLRESKGQISAANADAMGFNAYNGGGAKQIIFASSI 396
           SLRESKGQISAANADAMGFNAYNGGGAKQIIFASSI
Sbjct: 361 SLRESKGQISAANADAMGFNAYNGGGAKQIIFASSI 396
```

tr Q46009 **Flagellin [Campylobacter coli]** 572 AA
align

```
 Score =  724 bits (1869), Expect = 0.0
 Identities = 385/396 (97%), Positives = 389/396 (98%), Gaps = 1/396 (0%)

Query: 1   GFRINTNVAALNAKANSDLNSRALDQSLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
           GFRINTNVAALNAKANSDLNSRALDQSLSRLSSGLRINSAAD ASGMAIADSLRSQANTL
Sbjct: 2   GFRINTNVAALNAKANSDLNSRALDQSLSRLSSGLRINSAADVASGMAIADSLRSQANTL 61

Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120
           GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAA+DGQSLKTRTMLQADINRLME
Sbjct: 62  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAEDGQSLKTRTMLQADINRLME 121

Query: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 180
           ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTR    ++ F
Sbjct: 122 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRLNRFTK-F 180

Query: 181 SSGTVGLTIKNYNGIEDFKFDSVVISTSVGTGLGALAEEINRNADKTGIRATFDVKSVGA 240
           SSGTVGLTIKNYNGIEDFKFDSVVISTSVGTGLGALAEEINRNADKTGIRATFD+KSVGA
Sbjct: 181 SSGTVGLTIKNYNGIEDFKFDSVVISTSVGTGLGALAEEINRNADKTGIRATFDLKSVGA 240

Query: 241 YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLVLTS 300
           YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLVLTS
Sbjct: 241 YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLVLTS 300

Query: 301 ADGRGIKITGSIGVGAGILHTENYGRLSLVKNDGRDINISGTGLSAIGMGATDMISQSSV 360
           ADGRGIKITGSIGVGAGILHTENYGRLSLVKNDGRDINISGTG SAIGMGATDMISQSSV
Sbjct: 301 ADGRGIKITGSIGVGAGILHTENYGRLSLVKNDGRDINISGTGFSAIGMGATDMISQSSV 360

Query: 361 SLRESKGQISAANADAMGFNAYNGGGAKQIIFASSI 396
           SLRESKGQISAANADAMGFNAYNGGGAKQIIFASSI
Sbjct: 361 SLRESKGQISAANADAMGFNAYNGGGAKQIIFASSI 396
```

sp P18245 **Flagellin B (Flagellin N) [flaB] [Campylobacter coli]** 572 AA
FLAB_CAMCO

align

tr Q9RPY6 **Flagellin A [flaA] [Campylobacter jejuni]** 574 AA
align

Score = 722 bits (1863), Expect = 0.0
Identities = 379/396 (95%), Positives = 388/396 (97%), Gaps = 2/396 (0%)

```
Query: 1   GFRINTNVAALNAKANSDLNSRALDQSLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
           GFRINTNVAALNAKANSDLNSRALDQSLSRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 2   GFRINTNVAALNAKANSDLNSRALDQSLSRLSSGLRINSAADDASGMAIADSLRSQANTL 61

Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120
           GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME
Sbjct: 62  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 121

Query: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 180
           ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF
Sbjct: 122 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 181

Query: 181 SSGTVGLTIKNYNGIEDFKFDSVVISTSVGTGLGALAEEINRNADKTGIRATFDVKSVGA 240
           SSGTVGLTIKNYNGIEDFKFDSVVISTSVGTGLGALAEEINRNADKTGIRATFDVKSVGA
Sbjct: 182 SSGTVGLTIKNYNGIEDFKFDSVVISTSVGTGLGALAEEINRNADKTGIRATFDVKSVGA 241

Query: 241 YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLVLTS 300
           YAIKAGNTSQDFAINGVVIG+++Y+DGD NG LISAINAVKDTTGVQASKDENGKLVLTS
Sbjct: 242 YAIKAGNTSQDFAINGVVIGQINYNDGDNNGQLISAINAVKDTTGVQASKDENGKLVLTS 301

Query: 301 ADGRGIKITGSIGVGAGILHTENYGRLSLVKNDGRDINISGTGLSAIGMGATDMISQSSV 360
           ADGRGIKITGSIGVGAGILHTENYGRLSLVKNDGRDINISGTGLSAIGMGATDMISQSSV
Sbjct: 302 ADGRGIKITGSIGVGAGILHTENYGRLSLVKNDGRDINISGTGLSAIGMGATDMISQSSV 361

Query: 361 SLRESKGQISAANADAMGFNAYNGGGAKQIIFASSI 396
           SLRESKGQISAANADAMGFN+Y GGG  + +F  ++
Sbjct: 362 SLRESKGQISAANADAMGFNSYKGGG--KFVFTQNV 395
```

tr Q99QL6 **Flagellin A (Fragment) [flaA] [Campylobacter jejuni]** 574 AA
align

Score = 702 bits (1813), Expect = 0.0
Identities = 366/398 (91%), Positives = 385/398 (95%), Gaps = 2/398 (0%)

```
Query: 1   GFRINTNVAALNAKANSDLNSRALDQSLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
           GFRINTN AALNAKANSDLN+++LD SL+RLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 1   GFRINTNGAALNAKANSDLNAKSLDSSLARLSSGLRINSAADDASGMAIADSLRSQANTL 60

Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120
           GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LME
Sbjct: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120

Query: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 180
           ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQT+KA+IGATQSSKIGVTRFETGSQSF
Sbjct: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTVKATIGATQSSKIGVTRFETGSQSF 180

Query: 181 SSGTVGLTIKNYNGIEDFKFDSVVISTSVGTGLGALAEEINRNADKTGIRATFDVKSVGA 240
           +SG VGLTIKNYNGIEDFKFD+VVISTSVGTGLGALAEEIN+NADKTG+RAT+DVK+ GA
```

```
Sbjct: 181 TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKNADKTGVRATYDVKTTGA 240

Query: 241 YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLVLTS 300
           YAIKAG TSQDFAINGV+IGKVDY DGD NGSLISAINAVKDTTGVQASKDENGKLVLTS
Sbjct: 241 YAIKAGTTSQDFAINGVIIGKVDYKDGDNNGSLISAINAVKDTTGVQASKDENGKLVLTS 300

Query: 301 ADGRGIKITGSIGVGAGILHT--ENYGRLSLVKNDGRDINISGTGLSAIGMGATDMISQS 358
           ADGRGIKITG IGVG+GIL T  ENYGRLSLVKNDGRDIN+SGTGLSAIGMGA DMISQ+
Sbjct: 301 ADGRGIKITGDIGVGSGILSTQKENYGRLSLVKNDGRDINVSGTGLSAIGMGAADMISQA 360

Query: 359 SVSLRESKGQISAANADAMGFNAYNGGGAKQIIFASSI 396
           SVSLRESKGQISAANADAMGFN+YNGGGAKQI+ ASSI
Sbjct: 361 SVSLRESKGQISAANADAMGFNSYNGGGAKQILQASSI 398
```

tr Q99Q27 **Flagellin A (Fragment) [flaA] [Campylobacter jejuni]** 576 AA
align

```
 Score =  696 bits (1796), Expect = 0.0
 Identities = 365/400 (91%), Positives = 384/400 (95%), Gaps = 4/400 (1%)

Query: 1   GFRINTNVAALNAKANSDLNSRALDQSLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
           GFRINTN AALNAKANSDLN+++LD SL+RLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 1   GFRINTNGAALNAKANSDLNAKSLDSSLARLSSGLRINSAADDASGMAIADSLRSQANTL 60

Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120
           GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LME
Sbjct: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120

Query: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 180
           ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQT+KA+IGATQSSKIGVTRFETGSQSF
Sbjct: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTVKATIGATQSSKIGVTRFETGSQSF 180

Query: 181 SSGTVGLTIKNYNGIEDFKFDSVVISTSVGTGLGALAEEINRNADKTGIRATFDVKSVGA 240
           +SG VGLTIKNYNGIEDFKFD+VVISTSVGTGLGALAEEIN+NADKTG+RAT+DVK+ GA
Sbjct: 181 TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEEINKNADKTGVRATYDVKTTGA 240

Query: 241 YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLVLTS 300
           YAIKAG TSQDFAINGV+IGKVDY DGD NGSLISAINAVKDTTGVQASKDENGKLVLTS
Sbjct: 241 YAIKAGTTSQDFAINGVIIGKVDYKDGDNNGSLISAINAVKDTTGVQASKDENGKLVLTS 300

Query: 301 ADGRGIKITGSIGVGAGIL--HTENYGRLSLVKNDGRDINISGTGLSAIGMGATDMISQS 358
           ADGRGIKITG IGVG+GIL    ENYGRLSLVKNDGRDIN+SGTGLSAIGMGA DMISQ+
Sbjct: 301 ADGRGIKITGDIGVGSGILSAQKENYGRLSLVKNDGRDINVSGTGLSAIGMGAADMISQA 360

Query: 359 SVSLRESKGQISAANADAMGFNAYNGGGAKQI--IFASSI 396
           SVSLRESKGQISAANADAMGFN+YNGGGAKQI  + ASSI
Sbjct: 361 SVSLRESKGQISAANADAMGFNSYNGGGAKQILQVQASSI 400
```

tr Q93NL6 **Flagellin A (Fragment) [flaA] [Campylobacter jejuni]** 557 AA
align

```
 Score =  687 bits (1774), Expect = 0.0
 Identities = 358/389 (92%), Positives = 377/389 (96%), Gaps = 2/389 (0%)
```

```
Query: 10  ALNAKANSDLNSRALDQSLSRLSSGLRINSAADDASGMAIADSLRSQANTLGQAISNGND 69
           ALNAKANSDLN+++LD SL+RLSSGLRINSAADDASGMAIADSLRSQANTLGQAISNGND
Sbjct: 1   ALNAKANSDLNAKSLDSSLARLSSGLRINSAADDASGMAIADSLRSQANTLGQAISNGND 60

Query: 70  ALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLMEELDNIANTT 129
           ALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LMEELDNIANTT
Sbjct: 61  ALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLMEELDNIANTT 120

Query: 130 SFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSFSSGTVGLTI 189
           SFNGKQLLSGGFTNQEFQIGSSSNQT+KA+IGATQSSKIGVTRFETGSQSF+SG VGLTI
Sbjct: 121 SFNGKQLLSGGFTNQEFQIGSSSNQTVKATIGATQSSKIGVTRFETGSQSFTSGVVGLTI 180

Query: 190 KNYNGIEDFKFDSVVISTSVGTGLGALAEEINRNADKTGIRATFDVKSVGAYAIKAGNTS 249
           KNYNGIEDFKFD+VVISTSVGTGLGALAEEIN+NADKTG+RAT+DVK+ GAYAIKAG TS
Sbjct: 181 KNYNGIEDFKFDNVVISTSVGTGLGALAEEINKNADKTGVRATYDVKTTGAYAIKAGTTS 240

Query: 250 QDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLVLTSADGRGIKIT 309
           QDFAINGV+IGKVDY DGD NGSLISAINAVKDTTGVQASKDENGKLVLTSADGRGIKIT
Sbjct: 241 QDFAINGVIIGKVDYKDGDNNGSLISAINAVKDTTGVQASKDENGKLVLTSADGRGIKIT 300

Query: 310 GSIGVGAGILHT--ENYGRLSLVKNDGRDINISGTGLSAIGMGATDMISQSSVSLRESKG 367
           G IGVG+GIL T  ENYGRLSLVKNDGRDIN+SGTGLSAIGMGA DMISQ+SVSLRESKG
Sbjct: 301 GDIGVGSGILSTQKENYGRLSLVKNDGRDINVSGTGLSAIGMGAADMISQASVSLRESKG 360

Query: 368 QISAANADAMGFNAYNGGGAKQIIFASSI 396
           QISAANADAMGFN+YNGGGAKQI+ ASSI
Sbjct: 361 QISAANADAMGFNSYNGGGAKQILQASSI 389
```

tr Q93NL9 **Flagellin A (Fragment) [flaA] [Campylobacter jejuni]** 557 AA
align

```
 Score =  687 bits (1773), Expect = 0.0
 Identities = 358/389 (92%), Positives = 377/389 (96%), Gaps = 2/389 (0%)

Query: 10  ALNAKANSDLNSRALDQSLSRLSSGLRINSAADDASGMAIADSLRSQANTLGQAISNGND 69
           ALNAKANSDLN+++LD SL+RLSSGLRINSAADDASGMAIADSLRSQANTLGQAISNGND
Sbjct: 1   ALNAKANSDLNAKSLDSSLARLSSGLRINSAADDASGMAIADSLRSQANTLGQAISNGND 60

Query: 70  ALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLMEELDNIANTT 129
           ALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LMEELDNIANTT
Sbjct: 61  ALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLMEELDNIANTT 120

Query: 130 SFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSFSSGTVGLTI 189
           SFNGKQLLSGGFTNQEFQIGSSSNQT+KA+IGATQSSKIGVTRFETGSQSF+SG VGLTI
Sbjct: 121 SFNGKQLLSGGFTNQEFQIGSSSNQTVKATIGATQSSKIGVTRFETGSQSFTSGIVGLTI 180

Query: 190 KNYNGIEDFKFDSVVISTSVGTGLGALAEEINRNADKTGIRATFDVKSVGAYAIKAGNTS 249
           KNYNGIEDFKFD+VVISTSVGTGLGALAEEIN+NADKTG+RAT+DVK+ GAYAIKAG TS
Sbjct: 181 KNYNGIEDFKFDNVVISTSVGTGLGALAEEINKNADKTGVRATYDVKTTGAYAIKAGTTS 240

Query: 250 QDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLVLTSADGRGIKIT 309
           QDFAINGV+IGKVDY DGD NGSLISAINAVKDTTGVQASKDENGKLVLTSADGRGIKIT
Sbjct: 241 QDFAINGVIIGKVDYKDGDNNGSLISAINAVKDTTGVQASKDENGKLVLTSADGRGIKIT 300
```